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(FILE 'HOME' ENTERED AT 12:08:36 ON 05 APR 2004)

FILE 'DISSABS, 1MOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX, COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN, MEDICONF, PASCAL, PAPERCHEM2, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT, ADISNEWS, ANABSTR, BIOBUSINESS, BIOCOMMERCE, ...' ENTERED AT 12:08:46 ON 05 APR 2004

E 'SAINT-REMY' 'JEAN-MARIE'?/AU E SAINT-REMY JEAN-MARIE?/AU E JACQUEMIN MARC?/AU

WEST Search History

Hide Items Restore Clear Cancel

DATE: Monday, April 05, 2004

Hide?	Set Name	Query	Hit Count
	DB=PGPB	B, USPT, USOC, EPAB, JPAB, DWPI; THES=ASSIGNEE; PLUR=YI	ES; OP=ADJ
	L13	L11 same l4	5
	L12	L11 same l3	2
	L11	hemophilia adj a	839
	L10	L6 same l4	1
	L9	L5 same l4	159
	L8	L5 same 13	8
	L7	L6 same 13	1
	L6	(anti or antibod\$) adj L5	275
	L5	factor adj (VIII or V)	8473
	L4	sepsis or septic or thrombus	36439
Acceptant 1	L3	(systemic inflammatory response syendrome) or SIRS	40826
	L2	Jacquemin-marc-\$.in.	4
	L1	'Saint-remy'-'Jean-Marie'-\$.in.	4

END OF SEARCH HISTORY

ANSWER 8 OF 20 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5

ACCESSION NUMBER: 1999:465724 CAPLUS

DOCUMENT NUMBER: 131:115050

Antibodies against factor VIII in patients with solid TITLE:

tumors. Successful treatment of cancer may suppress

inhibitor formation

Sallah, Sabah; Singh, Paramjeet; Hanrahan, L. Robert AUTHOR(S): CORPORATE SOURCE:

Department Medicine, Division Hematology/Oncology,

Univ. Tennessee, Memphis, TN, 38163, USA

Haemostasis (1998), 28(5), 244-249 SOURCE:

CODEN: HMTSB7; ISSN: 0301-0147

PUBLISHER: S. Karger AG

Journal DOCUMENT TYPE: English LANGUAGE:

In 1995-1998, the authors treated 5 patients with anti-factor VIII antibodies and spontaneous bleeding. All patients had underlying malignant conditions. Initial control of the bleeding episodes and reduction in inhibitor titer was achieved in all patients. Disappearance of factor VIII inhibitor occurred in 3 patients after either resection of the tumor or chemotherapy. Immunosuppression therapy failed to eradicate the antibody in 2 patients with metastatic disease. Antibodies against factor VIII appearing in certain patients may be directly associated with the underlying malignancy, rather than a coincidental finding. Attempts to reduce the titer or eradicate the inhibitor may fail if recognition of the underlying condition is not sought, or an appropriate treatment of cancer is not offered. Antibodies against factor VIII developing in previously healthy individuals constitute the most common spontaneous inhibitors of any clotting factor. Accurate ests. of the incidence of antifactor VIII inhibitors are not available, since some of these antibodies may not be associated with bleeding, or the condition may be misinterpreted as disseminated intravascular coagulation, especially when it is associated with known underlying malignancy. About 50% of anti-factor VIII antibodies developing in the nonhemophilic population occur in otherwise healthy individuals over the age of 50 yr. Other conditions associated with the development of these inhibitors, in decreasing frequency, include autoimmune diseases, peripartum period, lymphoproliferative disorders, solid tumors and reaction to certain medications [1]. Patients with antibodies against factor VIII usually present with spontaneous bleedings involving soft tissues, retropharyngeal or retroperitoneal spaces, intracerebral or other types of serious hemorrhagic episodes. The most common laboratory abnormality is prolongation of PTT and decreased to absent factor VIII activity. Among the most commonly used products to manage patients with bleeding episodes and autoantibodies against factor VIII are high-dose human factor VIII, and inhibitor by-passing agents. Decreasing the inhibitor titer may also be achieved via plasma exchange and immuno-suppression. The formation of factor VIII antibodies in patients with solid tumors in terms of its course, response to treatment, and prognosis has not been addressed. We describe in this article the occurrence and the course of anti-factor VIII antibodies in 5 patients with solid malignancies.

THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS REFERENCE COUNT: 8 RECORD. ALL CITATIONS AVAILABLE IN T

L6 ANSWER 3 OF 20 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:70012 CAPLUS

DOCUMENT NUMBER: 135:32107

AUTHOR(S):

PUBLISHER:

TITLE: Transient factor VIII inhibitor in a hemophilia

patient after staphylococcal septic shock syndrome Yamamoto, Kazuhiko; Niiya, Kenji; Shigematu, Terunobu;

Kiguchi, Toru; Takenaka, Katsuto; Shinagawa, Katsushi;

Ishimaru, Fumihiko; Ikeda, Kazuma; Shima, Midori;

Harada, Mine

CORPORATE SOURCE: Second Department of Medicine, Okayama University

Medical School, Okayama, 700-8558, Japan

SOURCE: International Journal of Hematology (2000), 72(4),

517-519

CODEN: IJHEEY; ISSN: 0925-5710 Carden Jennings Publishing

DOCUMENT TYPE: Journal LANGUAGE: English

AB We report a transient type I factor VIII inhibitor that arose in a 30-yr-old hemophilia patient just after staphylococcal septicemia. This situation usually occurs early in the course of substitution therapy with factor VIII concentrate in hemophilia patients. Although disseminated intravascular coagulation and acute respiratory distress syndrome developed after septic shock, the patient recovered following i.v. administration of antibiotics (meropenem and gentamycin), an antithrombin preparation, high-dose methylprednisolone, and recombinant factor VIII concentrate

(rFVIII). During this therapy, however, activated partial thromboplastin time gradually lengthened. On the seventh day of hospitalization, intracranial hemorrhage occurred with right hemiplegia, even though the substitution therapy had continued at the same dosage (30 U/kg per day) of rFVIII. At that point, 4 Bethesda units of the type I inhibitor against factor VIII were detected in the plasma. Increased amts. (46 U/kg per day) of rFVIII and prednisolone were administered, and hypothermic therapy was initiated. Following these treatments, the patient's general condition gradually improved, and within 25 days the inhibitor titer dropped to undetectable levels and did not recur during treatment. These clin. findings suggest that the staphylococcal septic shock may have acted as a trigger in the development of transient factor VIII inhibitor in this patient.

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OM protein - pr	OM protein - protein search, using sw model
Run on:	April 5, 2004, 13:36:42 ; Search time 12.824 Seconds (without alignments) 575.678 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-044-569B-8 738 1 METPAQLLFLLLLWLPDTTGTKVEIKRTVAAPSVFIFPPS 143
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

389414 segs, 51625971 residues

Searched:

Issued Patents AA:*
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3: /cgn2 6/ptodate/2/iaa/6A_COMB.pep:*
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5: /cgn2 6/ptodate/2/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodate/2/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodate/2/iaa/PCTUS_COMB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 65, Application US/09472087; Patent No. 6682736; GENERAL INFORMATION: APPLICANT: HANSON, DOUGLAS C. APPLICANT: NEVEU, MARK J.

Sequence 17, Appl Sequence 18, Appl Sequence 21, Appl Sequence 21, Appl Sequence 183, Appl Sequence 153, Appl Sequence 153, Appl Sequence 153, Appl Sequence 20, Appl Sequence	1
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US-09-535-832A-17 US-09-472-087-88 US-08-862-124-14 US-09-472-087-21 US-09-472-087-93 US-08-276-862-153 US-08-276-862-153 US-08-899-575-153 US-08-899-575-153 US-08-807-75-153 US-08-807-75-153 US-08-807-75-163 US-08-807-75-163 US-08-807-75-16 US-09-472-087-90 US-09-472-087-90 US-09-472-087-91 US-09-472-087-91 US-09-472-087-91 US-09-472-087-91 US-09-472-087-91 US-09-472-087-91 US-09-472-087-91 US-09-472-087-91	
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90.3%; Score 666.5; DB 4; Length 235;
Best Local Similarity 91.6%; Pred. No. 1.3e-55;
Matches 131; Conservative 5; Mismatches 6; Indels 1
                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NEVEU, MARK J.
APPLICANT: NEVEU, MARK J.
APPLICANT: HUELER, EILLEN E.
APPLICANT: HUELLER, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFRENCE: ABX-PERS.
CURRENT FILING DATE: 1999-12-23
FRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 14
LENGTH: 235
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             ; Sequence 14, Application US/09472087; Patent No. 6682736; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-472-087-14
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US-09-472-087-65
US-09-472-087-14
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61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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US-08-862-124-5
US-08-862-124-5
Sequence 5, Application US/08862124
Settle No. 620153
APPLICANT: Dan, Michael D.
APPLICANT: Matti, Pradip K.
APPLICANT: Matti, Pradip K.
APPLICANT: Matti, Pradip K.
APPLICANT: SPECIFICALIZE DETECT CANCER CELLS, NUCLEOTIDES ENCOLTITLE OF INVENTION: PRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND TITLE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SECUENCES: 28
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: MUELER, EILLEN E.
APPLICANT: MUELER, EILLEN E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GENERRY
APPLICANT: CORVALAN, JOSE R.
ITITE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: 1999-12-23
FRIOR PILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTHARE: PALENTIN Ver. 2.1
SEQ ID NO 67
LENGTH: 233
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91.6%; Pred. No. 1.8e-54;
tive 2; Mismatches 7;
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STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 GGGTKVEIKRTVAAPSVFIFPPS 140
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Patent No. 6682736
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatibl
OPERATING SYSTEM: PC-DOS/N
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Best Local Similarity 91.6'
Matches 131; Conservative
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CORGANISM: Homo sapiens
US-09-472-087-67
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Pred. No. 1.8e-54;
2; Mismatches 7; Indels 3
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APPLICANT: HANKE, JEFFREY H.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CONVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILLE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: 60/113,647
PRIOR PILLING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFFWARE: PALENTIN VANCE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFFWARE: PALENTIN VANCE: 1508-12-23
NUMBER OF SEQ ID NOS: 147
             APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CRVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REPRESENCE: ABA. PF.
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 601113,647
PRIOR PILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PACENTIN VOR: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.3%; Score 666.5; DB 4; Best Local Similarity 91.6%; Pred. No. 1.3e-55; Matches 131; Conservative 5; Mismatches 6;
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Patent No. 6682736
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Best Local Similarity 91.6%;
Matches 131; Conservative
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
MUELLER, EILLEN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-09-472-087-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-472-087-15
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LENGTH: 233
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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28

ENCODING THE

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Sequence 69, Application US/03472087
Patent No. 6682736
GENERAL INFORMATION:
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// Patent No. 5744585
// Patent No. 5744585 5712371
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ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatibl
OPERATING SYSTEM: PC-DOS/W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-472-087-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Madison
                                                                                                                                                                                                                                                                                                                  US-09-472-087-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Sim
Matches 130;
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US-08-405-034-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS---AL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 MEFQAQLLFLLLLMLPDITGDIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQK 64
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: MUSLIER, BILLEN E.
APPLICANT: GILMAN, SIEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GOLVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABS.-PP1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
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Pred. No. 1.4e-53;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.0%; Score 649.5; DB 3;
87.7%; Pred. No. 3.2e-54;
tive 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ITFGGGTKVEIKRTVAAPSVFIFPPS 150
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                                                                                           FILING DATE: 22-MAY 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 31,943
REPERENCE/DOCKET NUMBER: 31,043
RELEPAN: (650) 813-560
FELEPAN: (650) 813-560
FE
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Best Local Similarity 90.9%;
Matches 130; Conservative
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Matches 128, Conservative
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 17
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CRGANISM: Homo sapiens
US-09-472-087-17
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TOPOLOGY:
US-08-862-124-5
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60 PGQAPRPLIYGVSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCQQYGISP-FTF 118
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APPLICANT: Medenica, Rajko D.
APPLICANT: Mikerjee, Sonjoy
TITLE OF INVENTION: Human Monoclonal Antibody Against Lung
TITLE OF INVENTION: Carcinoma
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: NEVEU, MARK J.
APPLICANT: HANKE, EILLEN E.
APPLICANT: HANKE, JEFFREN E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CONVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFRENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 6/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PATENTIN US: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.4%; Score 645; DB 4; Length 234; 90.9%; Pred. No. 1.4e-53;
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2; Mismatches
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                                                                                            121 GGGTKVEIKRTVAAPSVFIFPPS 143
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61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRVEPEDFAVXYCQQXDNS-VCTF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 METPAQLIFILILWIPDTTGEIVITQFPGTLSLSPGBRATLSCRASQSVASAYLAWYQQK
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Pred. No. 4.6e-48;
4; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/09456090A
| Sequence 42, Application US/09456090A
| Patent No. 6680209
| GENERAL INPORMATION:
| APPLICANT: Buechler, Joe
| APPLICANT: Unberg, Viet
| APPLICANT: Lonberg, Nils
| TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
| TITLE OF INVENTION: HUMAN ANTIBODIES, O99456,090A
| CURRENT FILIGATION NUMBER: US/09/456,090A
| CURRENT FILIG DATE: 1999-12-06
| NUMBER OF SEQ ID NOS: 110
| SOFTWARE: Patentin Ver. 2.1
| LENGTH: 226
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                                          41450-FWC-DIV
REGISTRATION NUMBER: 34,235
REFRENCE/DOCKET NUMBER: 4145
TELECOMMUNICATION INFORMATION:
TELEFRAX: 617-523-3400
TELEFAX: 617-523-6440
TELERAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGHH: 129 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.2%;
Matches 116; Conservative
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OCHANISM: Homo sapiens
CTHER INFORMATION: M1-5L
US-09-456-090A-42
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US-09-456-090A-42
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JS-64-BO-774A-4

JS-62-BO-6 4, Application US/08480774A

PATHOL NO. 5852186

GENERAL INFORMATION:
APPLICANT: WARASCO, Wayne A.
APPLICANT: WARASCO, Wayne A.
APPLICANT: POSNER, Marshall R.
TITLE OF INVENTION: ANTI-9p 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
TITLE OF INVENTION: AND USE THEREOF

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE BROOKE IN ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
CITY: BOSTON
STRATE: MA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
ZIP: USOS EDISCONER: WINDOWS Version 2.0
STREET: 130 WARE: 190 COMPATION OF MARSE: 190 CONDATION OF MARSE: 190 CONDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 81.8%; Score 604; DB 1; Length 134; Best Local Similarity 88.1%; Pred. No. 5.5e-50; Matches 118; Conservative 6; Mismatches 10; Indels
       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,034
                                                                                              FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/POCKET NUMBER: 34656.009
TELEPHONE: 608-831-2106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
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121 GOGTKLEIKRTVAA 134
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amino acid
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; MOLECULE TYPE: protein
US-08-405-034-4
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      Sequence 50, Application US/09456090A

Patent No. 6680209

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Mils
TITLE OF INVENTION:
TILE REFERENCE: 020015-0002000S

CURRENT FILICATION NUMBER: US/09/456,090A

CURRENT FILICATION NUMBER: 1999-12-06

NUMBER OF SEQ ID NOS: 110

SOFTWARE: PatentIn Ver. 2.1

LENGTH: 226
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Fatent No. 6680209

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunare
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HOMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
TITLE OF INVENTION: 1999-12-06
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110

SOFTWARE: PATENTIN Ver. 2.1
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Best Local Similarity 91.1%;
Matches 112; Conservative
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COTHER INFORMATION: M2-33L
US-09-456-090A-86
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
CTHER INFORMATION: M1-23L
US-09-456-090A-50
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US-09-456-090A-86
US-09-456-090A-50
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81 HRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKRTVAAPSVFIF 140
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Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Genare
APPLICANT: Valkirs, Gunare
APPLICANT: Lonberg, Nis
APPLICANT: Lonberg, Nis
APPLICANT: Lonberg, Nis
TITLE OF INFORMATION:
FILE REFERENCE: 020015-000200US
CURRENT FAPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SEQ ID NO 52
IENGTH: 224
                                                                  GENERAL INPORATION:
APPLICANT: BUCKLEY, JOE
APPLICANT: BUCKLEY, JOE
APPLICANT: BUCKLEY, JEEF
APPLICANT: Caray, Jeff
APPLICANT: Loriberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-0002000S
CURRENT FAPLICANTON NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 80
LENGTH: 226
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Pred. No. 2.1e-46;
6; Mismatches 7; Indels
US-09-456-090A-80
; Sequence 80, Application US/09456090A
; Patent No. 6680209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.1%;
89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.4
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
CTHER INFORMATION: M2-20L
US-09-456-090A-80
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; ORGANISM: HOMO SADiens
; OTHER INFORMATION: M1-25L
US-09-456-090A-52
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Best Local Similarity
Matches 112; Conserva'
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81 HRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKRTVAAPSVFIF 140

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81 HRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKRTVAAPSVFIF 140
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61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS--FTFGPGTKVDIKRTVAAAPSVFIF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 BIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQKPGQAPRLLIYGASSRATDIP 80
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                                                                                                                                                                     RESULT 15
US-09-456-090A-72
Squence 72, Application US/09456090A
SPELICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Cray, Jeff
APPLICANT: Lonberg, Nils
STILE REPERENCE: 02015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 72
ILENGTH: 226
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ORGANISM: Homo sapiens
CTHER INFORMATION: M2-11L
US-09-456-090A-72
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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 5, 2004, 13:25:01; Search time 12.1827 Seconds (without alignments) 1184.358 Million cell updates/sec Run on:

US-10-044-569B-2 788 1 MDWTWRILFIVAAATGTHAQ.......WVTVSSASTKGPSVFPLGSR 150 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Iq heavy chain V r	Ig heavy chain V r	₽	g mu cha	ery	g heavy chain pr	g heavy chain pr	g heavy chain V	g heavy chain V	g heavy chain pr	g heavy chain	g heavy	g heavy chain V	g heavy chain	g heavy	g heavy chain	heavy cha	g gamma-2a	b	g gamma	g heavy chain	g heavy chain	g gamma-	Ig heavy chain pre	g heavy chain				
SUMM	2362	3160	4953	1468	PL0105	3159	2925	1855	531680	HVHU35	S19245	S18553	PN0538	E1HUND	S18552	HVHUHG	S21924	PLOO11	S21916	A32483	826911	S37483	G2MS11	PT0371	C41287	N04	801321	07	2192
gt.	71	36	35	27	160 2	32	48	17	17	17	42	17	38	43	17	17	31	51	34	42	œ	σ	74	17	37	0	75	41	11
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chain	chain									chain				chain	chain
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831698	831667	S29594	836265	E32513	144151	MHMS18	S18554	826909	PH0952	A30577	D33548	846393	A27472	S04576	838950
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		178	118	138	126	139	117	86	128	135	123	129	131	136	246
116	116									52.2 135					
53.1 116	116	53.0	52.9	52.8	52.7	52.6	52.5	52.4	52.3		51.9	51.9	51.6	51.6	51.6

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Approcession: FLOW APPROCESSION FOR A MODE AND A MODE A
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: 12-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Accession: 81596
R.Quisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A.PBerription: Mechanisms that generate human immunoglobulin diversity operate from the A.Accession: 831596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: PL0105 Litwin, S.; Carmack, C.E. R;Silberstein, L.E.; Litwin, S.; Carmack, C.E. A; Extlaberstein, L.E.; Litwin, S.; Carmack, C.E. A; Extlab. Med. 169, 1631-1643, 1989 A; Fittle: Relationship of variable region genes expressed by a human B cell lymphoma sec A;Reference number: PL0106; MUID:89235583; PMID:2541221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
                                                                                                                                                                                                                                                                                                                                                              1 MDWTWSILFLVAAATGAHSQVQLVASGAEVNKPGASVKVSCKASGYTFTSYGISWVRQAP
                                                                                                                                                                                                                                   1 MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKASGGFFSSXAISWVRQAP
                                                                                                                                                                                                                                                                                                                           61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMBLSSLRSDDTAVYYCA---
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                                                                                                                                                                                         1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                              Gaps
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                                                               Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Indels
                                                                                                                          31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LGPYSSGWYPNSDYYYYGMDVWGQGTTVTVSSGSASAPTLFPLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 -----VPDPDAF----DIWGQGTMVTVSSASTKGPSVFPLGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YCSGGGCYRGD----DYWGQGTLVTVSSGSRSAPTLFPLVS
                                                        64.5%; Score 508; DB 2;
llarity 61.2%; Pred. No. 8.5e-35;
Conservative 17; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.8%; Score 503; DB 2;
63.4%; Pred. No. 5.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.4%; Pred. .v..
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 63.48
Matches 102; Conservative
                                                        Query Match
Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: PL0105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOGLEWMGWINPNSGGTNYAOKFOGRVTWTRDTSISTAYMELSRLRSDDTAVYYCA-RAR 119
                                                                                                                                                                                                                                                                                                                                                              61 GKGLEWVGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                     GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCAVPDP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Homo sapiens (man)
.Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                               1 MDWTWRILFLVAAATSAHSQVQLVQSGAEVKKPGASVKVSCRASGYTFTSYDINWVRQAT
                                                                                                                                                                                                                                   1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
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A,Residues: 1-627 «FRI»
A,Residues: 1-627 «FRI»
A,Residues: 1-627 «FRI»
C,Superfamily: immunoglobulin C region; immunoglobulin homology
C,Reywords: immunoglobulin, membrane protein
F,1-15/Domain: signal sequence #status predicted «SIG»
F,16-627/Product: Ig mu chain #status predicted «MAI»
                                                                                                                                                                 ;
;
                                                                                                  Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 135;
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                                                                                                                                                             Indels
                                                                                                                          .7e-36;
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                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or DM1/JH4b)
                                                                                                                                                             12; Mismatches
                                                                                    65.7%; Score 517.5; ilarity 74.3%; Pred. No. 2.7 Conservative 12; Mismatches
C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-Sm antibody VH chain (VH1/DK1
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120 TGYNYWGQGTLVTVSS 135
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Matches 100; Conserv
                                                                                           Query Match
Best Local Similarity
Matches 101; Conserv
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Ig heavy chain V region - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Sacession: S31680
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: S31585
A; Accession: S31680
A; Restence number: S31585
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-17 < CUI>A; Residues: 1-17 < CUI>A; Cross-references: EMBL: Z14213; NID: G37795; PIDN: CAA78582.1; PiD: g37796
C; Genetics: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology < INM>
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C,Species: Homo sapiens (man)

C,Species: Homo sapiens (man)

C,Accession: S00476; S34013

E,Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuh

EMBO, T., 1047-1051, 1988

A;Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain l

A;Reference number: S00476; MUID:88296408; PMID:2841108
       D.A.;
                                                        from
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A;Accession: 823625
A;Accession: 822625
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-117 < OLE>
A;Coss-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
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                                                                                                                                                                                                                      A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                           59.9%; Score 472; DB 2; L
77.6%; Pred. No. 1.4e-32;
iive 8; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.5%; Score 469; DB 2; L
75.9%; Pred. No. 2.5e-32;
tive 10; Mismatches 18;
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Best Local Similarity 75.9
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 90; Conserv
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Adcession. 1995 # #equence_revision 06-Jun-1997 # text_change 23-Jul-1999
C;Adcession. S18551; S23625
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; EMBO J. 10, 3641.3645; 1991
A;Fille: Physical map of the 3' region of the human immunoglobulin heavy chain locus: c A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Adcession: S18551
A;Adcession: S18551
A;Residues: 1-117.<SHI.>
A;Cross-references: EMBL:X62106; NID:937831; FIDN:CAA44016.1; FID:937832
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| GOSLEWMGWISVADGKTKYSQKFQDRVTITRDTSATTAYMEVRGLRSEDTAVYYCARSPR
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                                                        PID:930997
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                                                                                                                                                                          Length 132;
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                            A;Residues: 1-132 <CUI>
A;Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; Pl
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30; Indels
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                                                                                                                                                                     Query Match 61.0%; Score 480.5; DB 2; Best Local Similarity 69.9%; Pred. No. 3.2e-33; Matches 95; Conservative 11; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 476; DB 2;
; Pred. No. 8.5e-33;
14; Mismatches 30;
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62.2%;
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Best Local Similarity 62.2
Matches 92; Conservative
       A; Molecule type: mRNA
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Ig heavy chain V region precursor (VI-3b) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-dan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: 618553; 826916
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Rshin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; A;Title: Physical map of the human immunoglobulin heavy chain locus: c
A;Reference number: $18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region (clone LUNm03) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jan-2000
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jan-2000
C;Accession: PNO538
R;Avila, M.A.; Vazques, J.; Danielsson, L.; de Cossio, M.E.F.; Borrebaeck, C.A.K.
Gene 127, 273-274 1993
A;Atile: Sequence determination of variable region genes of two human monoclonal antibo
A;Reference number: PNO535; MUID:93273246; PMID:8500770
                                                                                                                                                                                                                                                                                                                                                                                          A)Residues: 1-117 cHI.>
A)Cross-references: EMBL:X62109
A)Cross-references: EMBL:X62109
B) Malks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 27, 776-799, 1992
A)Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A)Reference number: $26685; MUID:93021117; PMID:1404388
A)Reference number: $26916
A)Rolecule type: DNA
A)Residues: 20-117 < TONA
A)Residues: 20-117 < TONA
A)Residues: 20-117 < TONA
A)Residues: 20-117 < TONA
A)Cross-references: EMBL:Z12327; NID:932871; PIDN:CAA78197.1; PID:932872
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A.Rossidues: 1-138 AAVI>
A.S.Cross-references: GB:M97804; NID:g185373; FIDN:AAB18935.1; FID:g1669777
A.Note: the authors translated the codon CCA for residue 75 as Ser, GCC for residue
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
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C.Skeywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #statutus predicted'<SIG>
F;20-117/Produce: Ig heavy chain V region (VI-3b) #status predicted
F;34-117/Domain: immunoglobulin homology <IMM>
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65.2%; Pred. No. 1.1e-30;
tive 10; Mismatches 23;
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A,Status: translation not shown
A,Molecule type: DNA
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Best Local Similarity
Matches 90; Conserv
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Cipecies: Homo sapiens (man)
Cipace: 22.Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
Cipace: 22.Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
Cipacesion: 819245
Riticam, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
Rixicam, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
A; Reliance number: 819245
A; Fitle: Immunoglobulin V(H) clan and family identity predicts variable domain structure
A; Reference number: 819245; MUD: 92164649; PMID: 1537339
A; Residue: preliminary; translation not shown
A; Residues: 1-142 < KIR>
A; Residues: 1-142 < KIR>
A; Residues: 1-142 < KIR>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology < INMA>
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:X07448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
A;Cross-references: EMBL:X07448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
A;Cross-references: EMBL:X07448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
A;Antette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidid: sequence analysis of the variable domains of four hums
A;Reference number: $34001; MUID:93209281; PMID:7681398
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A)Map position: 14q32.33-14q32.33
A;Introns: 16,1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-17/Product: ign heavy chain V region (V35) #status predicted <MAT>F;34-117/Pomain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change
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Pred. No. 4.6e-31;
9; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 464; DB 1;
Pred. No. 6.6e-32;
8; Mismatches 20;
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Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 20-116 <MAR>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: IGHV@
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Length 117; 20; Indels

; DB 2; 1.4e-30;

11; Mismatches Score 448; Pred. No. 1

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1 MDWTWRILFLVAAAIGVHSQVQLVQSGAEVKKPGASVKVSCKASGYIFTSYAMHWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-19/Domain: signal sequence #status predicted <SIG>F;20-117/Product: Ig heavy chain V region (VI-3) #status predicted <WAT>F;34-117/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 73.3%;
Matches 85; Conservative 1:
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EIHUND

Igheavy chain precursor V-I region (Nd) - human (fragments)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000

C;Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000

C;Accession: A93333, A02026

R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G

R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G

R;Kenten, J. Acad. Sci. U.S.A. 79, 6661-6665, 1982

R;Title: Cloning and sequence determination of the gene for the human immunoglobulin eps

R;Reference number: A93933

R;Accession: A93933

A;Recidues: I-143 < KEN>

R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Ja-dan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
Ciscossion: 81855
Rishin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, B.; H. Bishin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, B.; H. A; Shin, E.K.; Matsuda, P.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, B.; H. A; Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: classification: 818552
A; Accession: 818552
A; Accession: 818552
A; Residua: translation not shown
A; Molecule type: DNA
A; Residua: translation not shown
A; Residua: 1-117 < SHI>
A; Cross-references: EMBL:X62107; NID:G37833; PIDN:CAA44017.1; PID:G37834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Reference number: A94418
A.Contents: annotation; partial sequence
A.Contents: annotation; partial sequence
A.Contents: annotation; partial sequence
A.Contents: annotation; partial sequence
A.Gone: this epsilon chain was isolated from a myeloma protein
C.Generics:
A.Gene: GDB:IGHV®
A.Gene: GDB:IGHV
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          61 AQKFQGRVTMTEDTPTDTASLELSRVRSEDTAVYYCVTGPPRLSELAIFGVVKRIRGPFD 120
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                           121 IWGQGTRVTVSSASTKGP 138
                                                                                                             125 IWGQGTMVTVSSASTKGP
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Scoring table:

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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EMBO J. 7:1047-1051(1988).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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ID HVIG HUMAN

STANDARD; PRT; 117 AA.

P23083;

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 10-OCT-2003 (Rel. 20, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DF 10-OCT-2003 (Rel. 42, Last annotation update)

OF 10-NOV-1991 (Rel. 42, Last annotation update)
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PIR; $00476; HYHU35.
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:lmmune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007596; Ig-v.
InterPro; IPR007596; Ig-v.
IRRNDG0406; IGv; I.
SWART; SM00406; IGv; I.
PROSTTE; PS50835; IG_LIKE; I.
SIGNAL
                                                            HV3L_HUMAN
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HV3U_HUMAN
HV3C_HUMAN
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HV3D_HUMAN
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HV3K HUMAN
HV01 CAICR
HV38 MOUSE
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rattus norv
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788
1 MDWTWRILFLVAAATGTHAQ........MVTVSSASTKGPSVFPLGSR 150
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P01760 P
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P01771
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                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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MOUSE
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Listing first 45 summaries
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Result No.

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HV07_MOUSE
  HV1B HUMAN
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(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel Dekker, New York (1978).

-!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP
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GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA 116
                          21-JUL-1986 (Rel. 01, Created)
LoCOT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 heavy chain N-1 region ND precursor (Fragments).
19 heavy capies (Human).
Eukaryota Metazona, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-83065234; PubMed-6815656; Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney C. Bell L.O., Gould H.J.; "Cloning and sequence determination of the gene for the human imminoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 1.
RIMUNOGlobulin V region; Signal; Pyrrolidone carboxylic acid.
SIGNAL 1 19
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IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
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GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0005823; F: antigen binding; NAS.
GO; GO: 0005855; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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                                                                                                                                                         STANDARD;
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                                                                                                                                                         HUMAN
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RESULT 3

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WEDDLINE=81144028; PubMed=6298778;
REChavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                  21-JUL-1986 (Rel. 01, Created)
10-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-I region HG3 precursor.
If hemo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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56.6%; Score 446; DB 1; Length 117;
Best Local Similarity 70.7%; Pred. No. 7.1e-35;
Matches 82; Conservative 11; Mismatches 23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
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117 AA
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GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003825; F:antigen binding; NAS.

GO; GO:0006855; P:immune response; NAS.

InterPro; IPR007110; IG-like.
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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PIR; A02024; HVHUHG.
STANDARD;
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SMART, SM0406; IGv
PROSITE; PS50835; I
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SEQUENCE FROM N.A.
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Conservative
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711
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Best Local Similarity
Matches 79; Consern
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SEQUENCE
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ID HV48 MOU
AC P03980;
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                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by, and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120
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                                                                                 "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                           MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDON MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
                  MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae, Musimae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEAVY CHAIN V REGION B1-8/186-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION B1-8/1
PRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1A6U; 27-MAY-98.
PDB; 1A6U; 27-MAY-98.
InterPro; IPR007110; Ig-like.
InterPro; IPR00716; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv.
Immunoglobulin V region; Signal; 3D-structure.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region S43 precursor.
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D SEGMENT.
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SEQUENCE FROM N.A.
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NON TER
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STATETETETETE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                      "Heavy chain variable region contribution to the NPb family of antibodies: sometic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANDOUS: THE GAMMA-2A CHAIN MENA WAS CLONED FROM A HYBRIDOW MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
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MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
MEDLINE-81234548; PubWed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-0CT-1986 (Rel. 02, Created)
23-0CT-1986 (Rel. 02, Last sequence update)
15-UTL-1998 (Rel. 38, Last annotation update)
15-UTL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region TEPC 1017 precursor.
19 heavy chain V region TEPC 1017 precursor.
Eukaryots, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
D SEGMENT.
JHZ SEGMENT.
BY SIMILARITY.
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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I.- MISCELLANEOUS: THIS GERMIINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
PIR, A02022; HWMS02.
HSSP, PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
                      Illegitimate recombination generates a class switch from C mu to
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1-JUL-1998 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last amocation update)
15-JUL-1999 (Rel. 38, Last amocation update)
1g heavy chain V region 102 precursor.
1g heavy claim V region 102 precursor.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mu
                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION TEPC 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.3%; Score 396; DB 1; Length 138; Best Local Similarity 55.1%; Pred. No. 4e-30; Matches 76; Conservative 20; Mismatches 40; Indels
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15576 MW; 748157E4C6907B8E CRC64;
                                        delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984)
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                                                                           PIR, A02033; HYMST7.
HSSP, P01810, 2FBJ.
INTEPEPO: IPR007110; Ig-like.
InterPro: IPR003596; Ig-v.
Pfam; PP00047; ig; 1.
SWART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LKE; 1.
Immunoglobulin V region; Signal.
SIGNAL.
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P01750;
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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                   FRAMEWORK-2.
COMPLENENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                                                                          Length 117;
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                FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Indels
IG HEAVY CHAIN V REGION 102.
                                                                                                                                                                                                                           31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12890 MW; 16191A088CB17F5A CRC64;
                                                                                                                                                  740A65DD851FCA8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.5%; Score 374; DB 1;
ilarity 59.5%; Pred. No. 3.7e-28;
Conservative 16; Mismatches 31;
                                                                                                                                                                                      Query Match
47.5%; Score 374; DB 1;
Best Local Similarity 59.0%; Pred. No. 3.7e-28;
Matches 69; Conservative 17; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV09 MOUSE STANDARD; PRT; 117 AA. P01753; P11271; 21-0TL-1986 [Rel. 01, Created) 01-0TL-1999 [Rel. 11, Last sequence update) 15-UTL-1999 [Rel. 38, Last annotation update) 19 heavy chain V region 186-1 precursor.
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BY SIMILARITY.
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MART; SM0406; 1Gv; 1.
PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                     12867 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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HV04 MOUSE
P01748;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AKSLEWIGVISTYNGNTSYNQKPKGKATMTVDKSSSTVHMELARLISEDSANLYCARYYG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                        GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSSTAYMQLHSLTSEDSAVYYCA 116
           GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVXYCA 116
                                                                                                                                                                                                                                                                       "Simultaneous expression of immunoglobulin mu and delta heavy chains by a clored B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes."; Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=8222262; PubMed=6806821;
Krapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.
Blattner F.R.;
                                                                                                                                                       Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION BCL1. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.3%; Score 373; DB 1;
52.9%; Pred. No. 5.5e-28;
ive 20; Mismatches 44,
                                                                                                                              21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                             136 AA
                                                                                                                                                   V region BCL1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; PO1772; ZFB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003166; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SMO0406; iGv. 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                  21-JUL-1986 (Rel. 01, Created)
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Best Local Similarity 52.9'
Matches 72; Conservative
                                                                                           STANDARD;
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135
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136 AA;
                                                                                                                                                     Ig heavy chain
                                                                                          MOUSE
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SEQUENCE
           61
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140 AA.

PRT;

STANDARD;

RESULT 10 HV02_MOUSE ID HV02_MOUSE AC P01746;

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=83152818; PubMed=6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:303-311(1982) -- SIMILARITY: Contains i immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION 93G7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, J00493, AAA38128.1; -.
PIR; A94264; HYNSG7.
HSSP, PO10810; JPBG7.
InterPro; IPR07110; Ig-like.
InterPro; IPR03596; Ig_v.
Pfam; PR0047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Imminglobulin V region; Hybridoma; Signal.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V region 93G7 precursor.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA.
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nes 70; Conservative
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                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                            "Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANEOUS: THIS GERMINE GENE BELCNGS TO A SET OF CLOSELY PERATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES. HISSP; PO1810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
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                        WEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
1-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region VH558 B4 precursor.
1g heavy chain V region Chordaea; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Wus.
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Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION 23.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 364; DB 1; Length 11; Pred. No. 3.2e-27; 18; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C530F829C906F69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAMEWORK-3
                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam, PF00047; ig; 1.
SMART, SMO0406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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Cell 40:271-281(1985).
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58.6%;
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
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117
117 AA;
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P06328;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GRGLEWIGNIDPNSGGTKYNEKFKSKATLIVDKPSSTAYMQLSSLISEDSAVYYC 115
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MOSI_TaxID=10090;
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MEDLINE=81245215; PubMed=6789211;
Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
Niersity of germ-line immunoglobulin VH genes.";
Nature 292:426-430(1981).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                              B4.
                                                                                                                                                                                       IG HEAVY CHAIN V REGION VH558
PRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEMORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION 108A. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12834 MW; B8862FAC67ABD345 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 360; DB 1;
; Pred. No. 7.6e-27;
17; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.-uuL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V region 108A precursor.
IGH-VJ558.
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SWART; SM00406; ig; 1.
PROSITE; PS50835; IGV: 1.
Immunoglobulin V region; Signal.
Pfam; PF00047; ig; 1.
SMART; SM00406; igv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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MGD, MGI:96486, IGh-VJ558.
InterPro, IPR007110, IG-like.
InterPro, IPR003596, IG.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%;
57.4%;
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117 AA;
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Best Local Similarity
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NON TER
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JU HV14_MOUSE

JU JUL414_M

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DT 21-JUL

DT 21-JUL

DT 12-JUL

SANDEN

RA MEBLI

RA GIVOL

DA BABLI

DR HSSP, DR HSS
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HVOS MOUSE
P01749;
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Best Local
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                                                                                          1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                     "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANBOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED: GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                               61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA 116
                                                Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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llarity 57.8%; Pred. No. 2.2e-26;
Conservative 15; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION 145.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
    Length 117;
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                                              Indels
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Query Match
Best Local Similarity 55.2%; Pred. No. 1.8e-26;
Matches 64; Conservative 20; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                           HV10_MOUSE STANDARD; PRT; 117 AA. P01754; P11270; 117 AA. P01754; P11270; 117 Created) 01-JUL-1986 (Rel. 01, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 28-FES-2003 (Rel. 41, Last annotation update) 1G heavy chain V region 145 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
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Best Local
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1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP

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-:- MISCELLANBOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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1 MGWSCIMLFLAATATGVHFQVQLQQPGAELVKPGASVKLSSKASGYTFTSYWMHWVKQRP
                                                       GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDIAVYYCA 116
                                                                                         61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYYQLSSLTSEDSAVYYCA 116
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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56.9%; Pred. No. 2.7e-26;
ive 19; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13016 MW; 427C861C53975EDC CRC64;
                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FED-2003 (Rel. 41, Last annotation update)
19-Revy chain V region 3 precursor.
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HSSP; POL810; ZFBJ.
MGD; MGI:96486; IGh-VJ558.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_V.
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                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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117 AA;
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Search completed: April 5, 2004, 13:24:55 Job time: 7.85279 secs

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RESULT 1.
Q9Y298
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096g64 homo sapien
09brv0 homo sapien
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08d814 mus musculu
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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ALIGNMENTS

Gaps InterPro; IPR003596; ISA.

InterPro; IPR003596; ISA. SEQUENCE FROM N.A.
MEDLINE=98322155; PubMed=9657749;
Jacquemin M.G., Vander Blst L.P.L.;
Mechanism and kinetics of factor VIII inactivation: study with an IgG4 monolonal antibody derived from a hemophilia A patient with inhibitor."; Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606; ö 100.0%; Score 788; DB 4; Length 150; ilarity 100.0%; Pred. No. 5.9e-66; Conservative 0; Mismatches 0; Indels 19 POTENTIAL. 150 16031 MW; 563D164AB22802D5 CRC64; Last sequence update)
Last annotation update) 150 AA Created) Q9Y298; 01-NOV-1999 (TrEMBLrel. 12, Created 01-NOV-1999 (TrEMBLrel. 12, Last se 01-OCT-2003 (TrEMBLrel. 25, Last an IGG VH protein precursor (Fragment) IGG VH. PRT; PRELIMINARY; Homo sapiens (Human) 150 AA; Query Match Best Local Similarity Matches 150; Conserv NON TER SEQUENCE Signal. SIGNAL Q9Y298

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121 GOVGDFDSWGQGTLVTVSSASTKGPSVFPL 150
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Best Local Similarity 66.04
Matches 101; Conservative
                                                                                                              PRELIMINARY;
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01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Homo sapiens (Human).
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MI Strausberg R.L., Peingold B.A., Grouse L.H., Derge J.G.,

Altaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hisieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hisieh F.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Hidards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Villalon D.K., Marny D.M., Sodesgren B.J., Lu X., Gibbs R.A.,

A Hidhards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Hidhards S., Worley K.C., Male S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Hidhards A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R Generation and initial analysis of more than 15,000 full-length human
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                      1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                               1 MDWIWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                           GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Last sequence update)
Last annotation update)
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broc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                  469 AA.
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Matches 101, Conservative
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Straubberg R.;
Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, BC000851, AAH09851.1;
RR; S15590; S1550.
RG; GO:0005622; C:intracellular; IEA.
RG; GO:00005700; F:transcription factor activity; IEA.
RG; GO:0000355; P:regulation of transcription, DNA-dependent; IEA.
RG; GO:0000355; P:regulation of transcription, DNA-dependent; IEA.
RICEPPO; IPRO00105; HTHARAC.
RICEPPO; IPRO0106; Ig_MHC.
RICEPPO; IPRO0106; Ig_MHC.
RICEPPO; IPRO0106; Ig_WHC.
RICEPPO; IPRO0106; Ig_V.
RYSITE; PS00041; HTH ARAC FAMILY_1; 1.
RROSITE; PS00041; HTH ARAC FAMILY_1; 1.
RROSITE; PS00290; IG_MHC; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA---
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 614;
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Prostate;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC005951; AAH05951.1; -.
HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.7%; Score 510; DB 4;
66.0%; Pred. No. 3.6e-39;
iive 17; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 VPDPDAFDIWGQGTMVTVSSASTKGPSVFPLGS
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us-10-044-569b-2.rspt

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PRELIMINARY;
                                                                                                                             1810060009Rik protein.
IGH-1 OR 1810060009RIK.
                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig;
SMART; SM00406; IGv
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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095978;
                           DD BREEF BRE
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Zheng S., Shao X.
"Identification and characterization of SNC66, a Ig-like gene which is down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the BNBL/GenBank/DDBJ databases.
EMBL, AF283666, AAL3687.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-like.
InterPro; IPR003596; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDWTWRLLFLVAAVTSAHSQEQLEQSGAEVTKPGASVKVSCKASGYTFIAYDINWVRQAP
                                                                                                                                                                                                                                                                                                            1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                   1 MDWTWSILFLVAAATGAQSQVHLVQSGAEVMSPGASVRVSCKTSGYAFHTYSIIWVRQAP
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                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sāpiens (Human).
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                        Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.3%; Score 467; DB 4; Length 497; 57.4%; Pred. No. 2.9e-35; ive 24; Mismatches 34; Indels
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LKE; 4.
PROSITE; P$500290; IG_MHC; 1.
SEQUENCE 497 AA; 53665 MW; F24D08DFASA663E5 CRC64;
                                                                                                                                                                         0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VPDPDAF----DIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSSCONDYYYYYMDVWGKGTTVTVSSASPTSPKVFPL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                 Query Match 60.7%; Score 478.5; DB 4; Best Local Similarity 60.8%; Pred. No. 2.5e-36; Matches 96; Conservative 13; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGGRGFGYNWFDPWGHGTLVTVSSASPTNPKVFPL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             497 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                     INTERFY: SMOAGY; ig; 4.
SMART; SMOAGO; ig; 4.
SMOART; SMOAGO; IGV; 1.
PROSITE; PSSO290; IG MIKE; 4.
HYPOTHETICAL PROCED:
SEQUENCE 500 AA; 54154 MW; 0
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.7.,
Best Coservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNC66 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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Q8WY24;
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RESULT

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A Rawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., & Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., & Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., & Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Ratel P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., & Schriml L., Staubli F., Suzuki R., Tomita M., Magner D., Washio T., & Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., & Brewnstein M.J., Bolt C., Fletcher C., Fujita M., Garibldi M., Adustoni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N., & Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Masaki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; ĪĠv; 1.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 1.
SEQUENCE 473 AA, $1699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                     Last sequence update)
Last annotation update)
   473 AA.
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                                                         Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Pancreas;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nacure 7 2010018; BA225349.1; -. PIR; S26746; S26746. HSSP; P01842; 7FAB. MGD; MGI:96443; Igh-1. InterPro; IPR003006; IghHC. InterPro; IPR003066; IghHC. InterPro; IPR003596; IghHC.
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                                                         17,
17,
25,
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Best Local Similarity 57.7%;
                                                         01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001)
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01-MAY-1999
01-OCT-2003
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095978
ID 09597
AC 09597
DT 01-M
DT 01-M
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61 GHGLEWIGEILPGSGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARRLG 120
                                                                                                                                                                                                    61 GKGLEWYGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP-D 119
                                                                                                                                                                      61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCAVPDP 120
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                                                                                                            1 MDWTWRVFCLLAVGPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAP
13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٦,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUB-Salivary gland;
Strausbeed R.;
Submitteed (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018315; AAH18315.1; -.
N MOJ; MOI: 96448; Igh-6.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00306; Ig_WHC.
InterPro; IPR0047; ig; 5.
RNART; SM00406; IGV.
RPROSITE; PS00290; IG/HC; 3.
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-MOG 212 variable gamma 2a (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
   36;
                                                                                                                                                                                                                                                                                  121 DAF-----DIWGOGTMVTVSSASTKGP 142
                                                                                                                                                                                                                                                                                                                                            121 ITFGGAVSKGFYYYGMDVWGQGTTVTVSSHPRPAP 155
   17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 PDAFDIWGOGTMVTVSSASTKGPSVFPLGS 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 20, C
(TrEMBLrel. 20, L
(TrEMBLrel. 25, L
      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002
01-OCT-2003
      68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBVDC9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8VDC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGG2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8VCX7
      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GQGLEWMGGIGPGVGSTWCAEKFQGRLTMTRNTSTTTVYMBLSRLRFEDTAVYFCGRGGR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                     Definition of the property of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Homo sapiens putative microfibrillar protein with Ig-like domain 3 mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

MRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY039025; AAK82649.1; -..

InterPro; IPR007110; Ig-like.

Pfam; PF00047; ig; 1.

SMART; SMO0405; ig/v.

PROSITE; PSS0835; IG LIKE; 1.

SEQUENCE 159 AA; I7497 NW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
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Pred. No. 2.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.9%; Score 464; DB 4; Length 15
Best Local Similarity 59.6%; Pred. No. 1.3e-35;
Matches 90; Conservative 17; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 POTENTIAL.
157
17304 MW, 86986EDDA84D88B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96QS0 PRELIMINARY, PRT, 159 AA. 096QS0; C1-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 VPDPDAFDIWGOGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 WRSGNYNGHWGQGTPVTVSSSSTKGPSVFPL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
      protein precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
157 1
157 AA;
                                                               Homo sapiens (Human)
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Tilson M.D.;
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Best Local Similarity
                                                                                                                                       MCBI TaxID=9606;
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NON TER SEQUENCE

SIGNAL Signal

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Gaps

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EMBL; BC028249; AAH28249.1;
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                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             F33932; F33932
PH1105; PH1105
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Best Local Similarity
                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                       121
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Q8K172;
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                                                                                                                                                                                                                                                                                                                                                             61 GHGLEWIGELLPGSGRINYNEKFKGKITFTADISSNTAYIQFSSLISEDSAVYYCANYGS 120
                                                                                                                                                                                                                                                                                                      09
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                                                                                                                                                                                                                                                                                                                  1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99IA6;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Musmusculus (Mouse).
Musmusculus (Apparental Mouse).
Musmusculus (Mouse).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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3
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                                                                                                                                                                                                                                                         56.5%; Score 445; DB 11; Length 168; 55.7%; Pred. No. 8.3e-34; Artive 21; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC03495. AAH03495.1; -. PIR; F33932, AAH03495.1; -. FIRSP; P01810; 2FBJ. InterPro; IPR07110; Ig-like. InterPro; IPR0031006; Ig-MHC. InterPro; IPR003006; Ig-WHC. InterPro; IPR003596; Ig-V. Pfam; PF00047; ig; 4. SWART; SMO0406; IG-V. PROSITE; PS00239; IG-IMKE; 4. PROSITE; PS00239; IG-IMKE; 4. PROSITE; PS00239; IG-IMKE; 4.
                                                                                                                              "Targefing T cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ416332; CAC94867.1;
InterPro; IRR007110; 1g-1ike.
InterPro; IRR0073596; Ig-v.
Ffam; PR00447; ig; 1.
SMART; SM00406; IGV.
BROSITE; PS0835; IG ILKE; 1.
NON_TER
                                                       STRAIN=BALB/c;
Chernajovsky Y.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                         NON_TER 168 168
SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l protein.
484 AA; 52567 MW; BEAEA4F9BCF582FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         121 SRWYFDVWGAGTTVTVSSTKTTAPSVYPL 149
                                                                                                                                                                                                                                                                                                                                                                                           121 DA--FDIWGOGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.78
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                       [2]
SEQUENCE FROM N.A.
STRAIN=BALB/c;
                                          SEQUENCE FROM N.A.
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SEQUENCE 46
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Q99LA6
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYXCA-VPD 119
                                61 GKGLKMYGWVNIETGESVYADDFKGRFAFSLETSASTIHLQINNLKNEDTATYFCARSDY 120
61 GKGLEWYGSFDPESGESIYAREPQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence AI893S85.
Mass musculus (Mouse)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Breast tumor;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003596; Ig cl.
InterPro; IPR003596; Ig v.
InterPro; IPR003596; Ig v.
SMART; SM00407; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS06935; IG LIKE; 4.
PROSITE; PS060290; IG MHC; 2.
SEQUENCE 482 AA, 52121 NW; A06FP083E771D084 CRC64;
                                                                                                                 D----AFDIWGOGTMVTVSSASTKGPSVFPL 147
                                                                                                                                               121 DYDIYAMDYWGQGTSVTVSSESARNPTIYPL 151
                                                                                                                                                                                                                                                                                                                482 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 PDAFDIWGQGTMVTVSSASTKGPSVFPL 147
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1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60

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51007 MW; EAA674C6BBC30783 CRC64;
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time : 34.9797 secs
  463 AA;
  SEQUENCE
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Q99L25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGWNCIILFLVATATGVHSQVQLQQPGAELVXPGASVKLSCKASGYTFTSYWMHWVKQRR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein.
Hypotherical protein.
Bukaryous, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae; Musilaria, LaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Straubberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004315; AAH03435.1; -.
R PIR, B45837; B45837.
R HSSP; P01842; 7FAB.
R MGD; MGI-96446; 1gh-4.
R InterPro; 1PR00110; 1g-1ike.
R InterPro; 1PR00110; 1g-1ike.
R InterPro; 1PR00110; 1g-1ike.
R InterPro; 1PR00110; 1g-1ike.
R SMART; SM00407; 1g; 3.
F FAM: PR00117; 1g; 13.
R SMART; RM00406; 1GV; 1.
R PROSITE; PSS0835; IG LIKE; 4.
R PROSITE; PSS0835; IG LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.3%; Score 435.5; DB 11; Length Best Local Similarity 56.7%; Pred. No. 1.2e-32; Matches 85; Conservative 18; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012207; AAH12207.1; -.
InterPro; IPR003596; Ig.v.
InterPro; IPR003596; Ig.v.
Fram; PP00047; ig; 2.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
Hypothetical protein.
SRQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
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121 YDAMDYWGQGTSVTVSSEPAREPTIYPL 148
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                                                                                                                       PRELIMINARY;
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Mus musculus (Mouse)
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SEQUENCE FROM N.A.
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Q99LC4;
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                                                                          RESULT 13
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61 BOGLEWIGYIYPRDGSTKYNEKPKGKATITADKSSSTAYMQLNSLTSEDSAVCFCSRGGS 120
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Q90125,
01-UUN-2001 (TEMBLrel. 17, Last sequence update)
01-UUN-2001 (TEMBLrel. 17, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
Sum sculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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A Strausberg R.; Strau
     DB 11; Length
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Query Match 55.1%; Score 434.5; DB 11; Length Best Local Similarity 54.0%; Pred. No. 2.9e-32; Matches 81; Conservative 25; Mismatches 41; Indels
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nes 81; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein April 5, 2004, 12:09:21 ; Search time 48.4772 Seconds (without alignments) 874.270 Million cell updates/sec Run on:

Title:

US-10-044-569B-2 788 1 MDWTWRILFLVAAATGTHAQ.........WVTVSSASTKGPSVFPLGSR 150 Perfect score:

Sequence:

Scoring table:

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

3: geneseqp2000s:*

4: geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

ion	Heavy cha	Human B02	Human pol	Human	Human		Anti-h	Human ant	Human imm	Human IGF	Monoclona	Heavy cha	Humanised	Human imm	Monoclona	Humanised	Human pol		Humanised	Mouse hum		Humanised	Mouse hum	Humanised	Humanised
Description	Aab47058	Aa018876	Aam41145	Aay24372	Aay24371	Aam39359	Aau74296	Ade28427	Aab36210	Aay96302	Aaw88464	Aaw48650	Aar77610	Aar66316	Abu08022	Aar77615	Aam39164	Aaw90935	Aaw90933	ADD74904	Abb74902	Aaw90934	Abb74903	Aaw90936	Abb74945
ID	AAB47058	AA018876	AAM41145	AAY24372	AAY24371	AAM39359	AAU74296	ADE28427	AAB36210	AAY96302	AAW88464	AAW48650	AAR77610	AAR66316	ABU08022	AAR77615	AAM39164	AAW90935	AAW90933	ABB74904	ABB74902	AAW90934	ABB74903	AAW90936	ABB74945
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% Query Match	100.0	100.0	81.9	79.6	79.4	78.3	74.9	73.7	71.5	69.2	68.4	68.0	68.0	67.9	67.5	66.8	9.99	9.99	9.99	9.99	9.99	66.5	66.5	66.4	66.4
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ALIGNMENTS

Monoclonal antibody, variable region, heavy chain, light chain, VH; VL, complementarity determining region, CDR; MAb; BO2C11; conformational peptope, factor VIII; KRIXI, von Willebrand factor, hemostasis, intravascular coagulation, arterial thrombosis, arterial restenosis; venous thrombosis; arteriosclerosis. Heavy chain variable region VH of BO2C11. Location/Qualifiers AAB47058 standard; protein; 150 AA 44. .53 /label= CDR1 68. .86 /label= CDR2 115. .125 /label= CDR3 99GB-00016450. 99US-0143891P. Jacquemin MG, Saint-Remy JR; 13-JUL-2000; 2000WO-EP006677. (LEUV-) LEUVEN RES & DEV VZW (first entry) WPI; 2001-138333/14. N-PSDB; AAC85451. WO200104269-A1. 14-JUL-1999; 14-JUL-1999; Homo sapiens 18-JAN-2001. 08-MAY-2001 AAB47058; Key Domain Domain Domain RESULT 1 AAB47058

Novel cell lines for producing monoclonal antibodies that bind to factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.

Example 5; Fig 6; 55pp; English.

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RESULT 3
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KRIXI can be used to inhibit the binding of factor VIII to von Willebrand factor in a dose dependant manner. The new cell line KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation arterial thrombosis, and attenuation of coagulation such as intravascular coagulation, arterial thrombosis, arterial restenois; venous thrombosis or arteriosclerosis, and attenuation of coagulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly in humans
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/label= CDR1
68 .86
/label= CDR2
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/label= CD
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Best Local Similarity 100.
Matches 150; Conservative
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GKGLEWVGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
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                                                                                                                                                                                                                                                            The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic inflammancory response syndrome (SIRS), sepsis, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an active ingredient a partial inhibitor of factor VIII, in admaxture with a carrier. Such inhibitors may include the antibodies BO2C11 and KRIXI. The present sequence is the heavy chain variable region of BO2C11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDWIWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
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                                                                 enarmaceutical composition for treating systemic inflammatory respons
syndrome, sepsis, septic shock and/or thrombus formation in
microvasculature in mammals, comprises a partial inhibitor of factor
VIII
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100.0%; Pred. No. 8.1e-61;
iive 0; Mismatches 0;
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2000US-00620312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
WPI; 2002-610270/66.
N-PSDB; AAL49254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200153312-A1
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25-APR-2000;
20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Simi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Qian XB, Yang Y,

Ma Y, Xue AJ,

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as alzheiner's, Parkinson's disease, Huntington's disease, amyotrophic lateral scherosis, and Shy-Drager Syndrome. Other uses include the cutivities such as: Immune system suppression, activin/inhibin activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                     nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; monoclonal antibody; connective tissue growth factor; CTGF; cell proliferation disorder; fibrosis; liver cirrhosis; nephritis; skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer; rheumatic vascular inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human monoclonal antibody against CTGF SEQ ID NO:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.9%; Score 645.5; DB 4
84.5%; Pred. No. 8.2e-48;
cive 8; Mismatches 14
                                                                                                                                                                                                           Example 2; SEQ ID NO 6076; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D-AFDIWGQGTMVTVSSASTKGPSVFPL 147
                               Asundi V, Chen R,
Wehrman T, Xu C,
R, Drmanac RT;
                                                                                                                                                                          central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY24372 standard; protein; 146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-JP005697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 125; Conservative
                                 Liu C, Asund
Wang Z, Wehrn
Goodrich R, I
                                                                                                    2001-442253/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
HYSEQ INC
                                                                                                                       N-PSDB; AAI60301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 535 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-1998;
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                                 Tang YT,
Wang J,
Zhou P,
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 (HXSE-)
                                                                                                                                                       Novel
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Indels

14; DB 4;

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AAX90020 to AAX90029 encode monoclonal antibodies which react with human connective tissue growth factor (CTGP). AAX24369 to AAX24378 represent these monoclonal antibodies. The antibodies are useful in the diagnosis, prevention and treatment of cell proliferation disorders in which CTGP is implicated, including fibrosis of lung, kidney, liver and other tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid arthritis; rheumatic vascular inflammation; hepatitis; and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                           61 GKGLEWYGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCA---V 117
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDCTWRIFFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGXTLTELSMHWVRQAP
                                                                                                               New monoclonal antibody reactive with connective tissue growth factor useful in the treatment of cell proliferation disorders.
                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, monoclonal antibody, connective tissue growth factor; CTGF, cell proliferation disorder; fibrosis; liver cirrhosis; nephritis; skin ulcer; keloid, rheumatoid arthritis; hepatitis; cancer; rheumatic vascular inflammation.
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                                                                                                                                                                                                                                                                                                                     Length 146;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human monoclonal antibody against CTGF SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                       DB 2;
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                                                  Takigawa M;
                                                                                                                                                                                                                                                                                                                     Score 627.5; DB 2
Pred. No. 7.1e-47;
7; Mismatches 13
                                                                                                                                                          Claim 17; Page 184-185; 212pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VTPWYFDYWGOGTLVTVSSASTKGPS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 PDPDAFDIWGQGTMVTVSSASTKGPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakamoto S,
                                                   Sakamoto S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY24371 standard; protein; 146
                                                                                                                                                                                                                                                                                                                       79.6%;
84.2%;
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98JP-00356183
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                         (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                   Tezuka K,
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N-PSDB; AAX90022.
                                                                             1999-430232/36.
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                              Sequence 146 AA;
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15-DEC-1998;
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                                                   Tamatani T,
                                                                                                                                                                                                                                                                                                                                     Best Local Sim
Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY24371;
                                                                                                                                                                                                                                                                                                                       Query Match
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                           Wang D;
Zhao QA;
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                           Ren F, Wa
Zhang J,
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N-PSDB; AAI58515
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                                                                                                                        AAX90020 to AAX90029 encode monoclonal antibodies which react with human connective tissue growth factor (CTGF). AAX24369 to AAX24378 represent these monoclonal antibodies. The antibodies are useful in the diagnosis, prevention and treatment of cell proliferation disorders in which CTGF is implicated, including fibrosis of lung, kidney, liver and other tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid arthritis; rheumatic vascular inflammation; hepatitis; and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA---V 117
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, Zhao (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDCTWRILFLVAAATGTHAQVQLVQFGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                    New monoclonal antibody reactive with connective tissue growth factor useful in the treatment of cell proliferation disorders.
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Zhang J,
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Yang Y,
                                                                                                                                                                                                                                                                                                                                               79.4%; Score 625.5; DB 2;
84.2%; Pred. No. 1.1e-46;
live 7; Mismatches 13;
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Wehrman T, Xu C, Xue AJ,
R, Drmanac RT;
                                                                                 Claim 17; Page 180-181; 212pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 PDPDAFDIWGQGTMVTVSSASTKGPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VTPWYFDYWGQGTLVTVSSASTKGPS 146
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03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
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                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 84.2
Matches 123, Conservative
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Wang Z, Wehr
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                       Sequence 146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia.
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Wang
Zhou
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with noctropic. Immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system, and as peripheral nervous system, as a peripheral nervous system, as a soleropathise and carral nervous system diseases, amyorrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RCSSTSCYHPLGY--WGQGTLVTVSSAPIKAPDVFPI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.3%; Score 617; DB 4; Best Local Similarity 77.1%; Pred. No. 2.4e-45; Matches 121; Conservative 10; Mismatches 14
                                                                                                                                 Example 4; SEQ ID NO 2504; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU74296 standard; protein; 470 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-2001; 2001WO-JP004035.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200187981-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU74296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                             The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, for inducing antibody-dependent cytokine from AILIM-expressing cells, and for inducing antibody-dependent cytocoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells. (I) is useful for treating, preventing or prophylaxis of delayed type allergy. (I) is useful for treating and control diseases associated with AILIM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the diseases. (I) is useful for suppression, prevention and/or treatment of chemated arthritis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; variable region heavy chain; 21.2-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      psoriasis, autoimmune or allergic disorders, inflammation, graft versus host reaction, graft versus host disease, immune rejection, disorders host reaction, graft versus host disease, immune rejection, disorders caused by abnormal intestinal immunery, specifically inflammatory intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatitis. (I) induces no serious immunersjection due to antigenicity to human, i.e., human anti-mouse antigenicity (HAMA) in a host. AAU74296-AAU74201 represent anti-human AILIM monoclonal antibody amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAP
                                                                                                                                                                 New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human anti-CD40 antibody 21-2-1 variable region heavy chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.9%; Score 590; DB 5; Length 470; 75.5%; Pred. No. 4.7e-43; ive 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YDSSGYYHDAFDIWGQCTMVTVSSASTKGPSVFPL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                     Claim 30; Page 264-266; 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE28427 standard; protein; 471
18-MAY-2000; 2000JP-00147116
30-MAR-2001; 2001JP-00099508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004 (first entry)
                                                  (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 75.5
Matches 117, Conservative
                                                                                  Tezuka K,
                                                                                                                  WPI; 2002-075313/10
                                                                                                                                    N-PSDB; AAS99472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 470 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE28427;
                                                                                  Tsuji T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacerial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody variable region heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GKGLEWYGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTBLPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------DAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.7%; Score 580.5; DB 7; 72.4%; Pred. No. 3.2e-42; ive 11; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGYCTNGVCSYFDYWGQGTLVTVSSASTKGPSVFPL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated protein HISAP-8.
                                                                                                                                                                                                                                                                                                                                                                                                           Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 34; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           Corvalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36210 standard; protein; 467
                                                                                                                                                                                        08-NOV-2002; 2002WO-US036107.
                                                                                                                                                                                                                                                 09-NOV-2001; 2001US-0348980P
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Matches 113; Conservative
                                                                                                                                                                                                                                                                                                             (PFIZ ) PFIZER PROD INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                           Bedian V, Gladue RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-441521/41.
N-PSDB; ADE28426.
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                                                               WO2003040170-A2
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Homo sapiens
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                                                                                                                            15-MAY-2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36210;
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The present sequence is the human immunoglobulin superfamily protein IGFAM-14. Its gene was isolated from a cDNA library of gallbladder tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for disponents (such as inflammation, AIDS, allergies, anneamia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's dispase, diabetes mellitus, emphysema, fraves' disease, hepatitis, complications of cancer, haemodialalysis and ulcerative colitis), complications of cancer, haemodialalysis and extracorporeal circulation, trauma and haematopoletic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma; lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDWIWRILFLVAAATGIHAQVQLVQSGABVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                   Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody 4B5 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.2%; Score 545.5; DB 3;
69.7%; Pred. No. 1.5e-39;
ive 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SSPVGDAFDÍWGÓGTMVTVSSASPTSPKVFPL 152
                                                                                                                                                                                                                 Guegler KJ,
Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VPDPDAFDIWGQGTMVTVSSASTKGPSVFPL
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 88-89; 105pp; English.
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                                                                                           98US-00195853.
98US-0113635P.
99US-0128194P.
                                                         99WO-US027566
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                                                                                                                                                                                                                   Corley 1
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                                                                                                                                                                             (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                             2000-387796/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                N-PSDB; AAA27394
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                                                       19-NOV-1999;
                                                                                                                 22-DEC-1998;
07-APR-1999;
                                                                                                19-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1999
                   25-MAY-2000
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Best Local S
                                                                                                                                                                                                                                        Lu DAM,
                                                                                                                                                                                                                 Yue H,
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                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPs). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDs, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, theumatoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:||||;|
|GQGLEWMGGLAPENGEAVYAQKFLGRLTLSEDTSADTAYMFLNNLGSEDSAIYYCARQHY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                            New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVQVSCTVSGFTLSDLSVHWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, immunoglobulin, IGFAM-14, IGFAM, immune disorder, cancer,
infection, inflammation, haematopoiesis, AIDS, allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.5%; Score 563.5; DB 4; Length 467; 73.0%; Pred. No. 9.5e-41; Live 19; Mismatches 20; Indels 1
                                                                                                                                                                             Baughn MR;
                                                                                                                                                                             Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFFFDFWGQGTMVTVSSASTKGPSVFPL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 D-AFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .19
/label=_signal_peptide
                                                                                                                                                                             Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20, .219
/label= IGFAM-14
34. .117
/label= Ig_domain
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 61-64; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96302 standard; protein; 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IGFAM-14 immunoglobulin.
                                                         98US-00049672.
                                                                                                98US-00049672,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 73.0
Matches 108; Conservative
                                                                                                                                                                          Yue H, Lal P,
                                                                                                                                    (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                      WPI; 2001-030926/04.
N-PSDB; AAC66526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200029583-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                         27-MAR-1998;
                                                                                                27-MAR-1998;
                                                                                                                                                                          Tang YT, Yu
Hillman JL,
                   24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96302;
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ò 유 ò Q AAY96302

9 9

Gaps

5,

Length 219; Indela

for

Baughn MR;

WO9902545-A2

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Oligo:cistronic expression vector - useful for production of, e.g. MAb425/TNF-~a or MAb425/IL-2 antibody fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Von Hoegen I, Burge C, Bruemmer W, Dunker R, Rieke E,
Hauser H, Mielke C;
                                                                                                                 Antibody-cytokine fusion protein; tricistronic vecto
TNF alpha; IL-2; IRES; internal ribosome entry site.
                                                                  Heavy chain of hmAb425 fused to TNF alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 15; 89pp; English
                       04-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERE ) MERCK PATENT GMBH
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N-PSDB; AAV18096.
                                                                                                                                                                                            Synthetic.
Homo sapiens.
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30-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                            WO9811241-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-1998
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Region
                                                                                                                                                                                                                                                                                                                                         Region
요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This polypeptide comprises the heavy chain variable region of the recombinant human monoclonal antibody (MAD) 4B5. 4B5 recognises carboniant human monoclonal antibody (MAD) 4B5. 4B5 recognises carboniant bulbodies specific for GD2 antigen antibodies specific for GD2 antigen antibodies specific for GD2 antigen antibodies peocific for GD2 antigen and or metastatic melanoma, breast adenocarcinoma, number of adenocarcinoma, small cell lump carcinoma, onch adenocarcinoma and denocarcinoma. The invention encompasses 4B5 derivatives with immunologic specificity for antibodies specific for GD2. These contropies specific for antibodies specific for GD2. These contropies panding fragments, comprise regions of the 4B5 cD8 or antibods by capture and isolated heavy and light chains (see also VDJ junction and regions spanning the 4B5 cD8. Other derivatives include fragments (see AAXOSSD1-54) encoding 4B5 antibody V regions are also provided, and therapeutic plasmids and vectors, including vaccinia virus vectors, comprising these contropies. 4B5 has been shown to mimic GD2, and is particularly cuseful in generating a host immune response to cancer. Products of the invention can be used in the detection and treatment of e.g. astrocytoma, collapsedendscolloma, pending adenocarcinoma, medullobascma, primitive neural collapse can collapse coll lung adenocarcinoma, medullobascma, primitive neural adenocarcinoma, epithelial adenocarcinoma, elements such a denocarcinoma, benecation and adenocarcinoma, collapse collapse collapse cancinoma, pending denocarcinoma, pending promocarcinoma, pending promocarcinoma, collapse 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GKGLEWYGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYC---- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                 New antibody 4B5 polynucleotides and polypeptides - used to develop products for the diagnosis and treatment of cancers and for prophylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDWIWRVIELVAAAISARSQVQLVQSGAEVKKFGASVKVSCKASGYIFISFDLNWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.4%; Score 539; DB 2; Length 476; 66.9%; Pred. No. 1.3e-38; ive 16; Mismatches 26; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 ----AVPDPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy to reduce risk of recurrence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 79-80; 83pp; English.
                                                                                                                                                                                              (NOVO-) NOVOPHARM BIOTECH INC
                                                                                                 98WO-IB001046,
                                                                                                                                             97US-0051945P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.99 hes 105; Conservative
                                                                                                                                                                                                                                                                                        WPI; 1999-120769/10.
N-PSDB; AAX06951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 476 AA;
                                                                                                                                                08-JUL-1997;
                                                                                                 08-JUL-1998;
                                                   21-JAN-1999
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Matches
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Welge T;

1. .494 /note= "Heavy chain of human mAb 425"

/note= "TNF alpha"

.652

97WO-EP004765. 96EP-00114820. 96EP-00115635.

Location/Qualifiers

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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a fusion protein comprising of TNF alpha fused to the C-terminus of the heavy chain of the human monoclonal antibody 425 (hmAb425). The hmAb425 has specificity for the human EGF receptor. The invention claims for a new pMCLDHAP tricistronic vector (AAV18036) for the expression of an antibody-cyckine fusion protein, hmAb422-TNF alpha. The TNF alpha sequence can be substituted by the IL-2 sequence. The vector alps contains a strong promoter/enhancer unit, a selection marker gene and at least two policyirus derived internal ribosomal entry site (IRES) sequences. The vector can be expressed in ammanian host cells for the production of heteromeric fusion proteins. This expression system is claimed to produce the heteromeric proteins in high yields
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              68.0%; Score 536; DB 2;
60.6%; Pred. No. 3.4e-38;
ive 14; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D----AFDIWGQGTMVTVSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.68
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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RESULT 13 AAR77610

AAW48650 standard; protein; 652 AA.

RESULT 12 AAW48650

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AAW48650;

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us-10-044-569b-2.rag

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Protein sequences (AAR66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAQ78339-7902) were isolated and cloned from a series of cosmid constructs: V202; V103; V21; Y6; V24; 3-31; M84; M18 and M31; by PCR amplification using primers AAQ78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with TaqI restriction enzyme. The fragments were iligation products were in vitro packed and infected into E.coli 490A. The fragments were hon subcloned by colony Mybridisation. The Vigaments encoding them are useful in producing human immemmalian hosts. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKGLEWMGGFDPEDGETIYAOKFQGRVTMTEDISTDTAYMELSSLRSEDTAVYYCA 116
                                                                                                                                                                                                              Primer, PCR, amplify, human, immunoglobulin, variable, heavy chain, cosmid, placenta, vector, pJB81, E.coli, mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.9%; Score 535; DB 2; L
87.9%; Pred. No. 6.1e-39;
ive 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising human immunoglobulin Vh human immunoglobulin in mammalian
                                                                                                                                                                                  Human immunoglobulin variable heavy chain #22.
      121 GSSPNWYFDVWGQGTLVTVSSASTKGPSVFPL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 33; Page 61-62; 130pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU08022
ID ABU08022 standard, protein; 476 AA.
                                                                             AAR66316 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                  93WO-JP000603.
                                                                                                                                                                                                                                                                                                                                                                               93WO-JP000603
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-006791/01.
N-PSDB; AAQ78962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA fragment c
production of
                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                               10-MAY-1993;
                                                                                                                                                                                                                                                                                        WO9426895-A1
                                                                                                                                     25-MAR-2003
03-AUG-1995
                                                                                                                                                                                                                                                                                                                    24-NOV-1994.
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                                                                                                          AAR66316;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                               AAR6631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:||||:| | || || || GGLEWMGEILFGSGSTEYAQKFQGRVTWTADTSTSTAYMELSSLRSEDTAVYYCARYFF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH + HGHRL (ARA77610), includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. It can be co-expressed with a humanised light chain (AAR77612) in human 293 EBNA cells using encoding DNAs subcloned into vector APEX-3P (AAT08476). Such humanised recombinant antibodies retain the ability of MAD 5G1.1 to block human complement C5s generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCA---- 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKWSWVILFILISVTAGVHSQVQLVQSGAEVKKPGASVKVSCKASGYIFSNYWIQWVRQAP
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C, Wang Y, Wilkins JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 249;
                                                                                                                                Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%; Score 535.5; DB 2 69.1%; Pred. No. 1.3e-38; ive 15; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 VPDPD-AFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 11; Page 119-122; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EE, Nye SH
Thomas TC,
                                                                                                                                                                                                                                                                    20. .249
/label= mat_peptide
45. .54
/label= CDR-H1
                                                                                                                                                                                                                                         .19
label= sig_peptide
                                                                                                                                                                                                                        Location/Qualifiers
AAR77610 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                               :9. .79
'label=_CDR-H2
                                                                                                                                                                                                                                                                                                                                                            118. .130
/label= CDR-H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evans MJ, Matis L, Mueller
Springhorn JP, Squinto SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US005688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-00236208
                                                                                                       Humanised 5G1.1 VH + IGHRL
                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 69.1%
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-392923/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT08483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     WO9529697-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-1994;
                                                          25-MAR-2003
15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-1995
                                                                                                                                                                                             Synthetic
                              AAR77610;
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                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                    Peptide
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The invention discloses a recombinant antibody comprising a constant region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable region. Rabies is an acute, neurological disease caused by infection of the central nervous system with the rabies virus, a member of the Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods for producing an isolate recombinant antibody by culturing a host cell, containing a recombinant entibody by culturing a host cell, molecule encoding the antibody. And isolating the nucleic acid molecule encoding the antibody varies of a pathogon by expressed and treating an individual exposed to a pathogon by antibodies are useful for preventing (vaccine) and treating an individual exposed to a pathogon, e.g. rabies infection. They are also useful for the qualitative determination of the rabies virus. The sequences presented are the antibody protein fragments, the nucleic acids encoding them or the PCR primers used to construct the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant antibody comprising a constant region of Mab 57 linked to a non-Mab 57 variable region, useful for treating an individual exposed to a pathogen, e.g. rabies infection.
                                                                                                                               Human; antibody; constant region; monoclonal antibody 57; Mab 57; variable region; Rabies; neurological disease; infection; central nervous system: rabies virus; Lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.5%; Score 532; DB 6; Length 476; 67.5%; Pred. No. 5.38-38; live 13; Mismatches 28; Indels
                                                                                              Monoclonal rabies virus antibody heavy chain, clone 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 38; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                   21-AUG-2002; 2002WO-US026584.
                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-2001; 2001US-0314023P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dietzschold B;
                                                      10-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-278566/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 476 AA;
                                                                                                                                                                                                                                                                     WO2003016501-A2.
                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hooper DC,
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61 GKGLEWVGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120 61 GQGLEWMGGIIPIFGTANYAQRFQGRLTITADBSTSTAYMELSSLRSDDTAVYFCARENL 120 1 MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKASGGTFNRYTVNWVRQAP 60 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60 121 DA-----FDIWGOGTMVTVSSASTKGPSVFPL 147 Best Local Similarity 67.5 Matches 106; Conservative ò g 8 ò

DNSGTYYYFSGWFDPWGQGTLVTVSSASTKGPSVFPL 157 121

5, 2004, 13:24:15

Search completed: April Job time: 50.4772 secs

Sequence 157, App Sequence 117, App Sequence 117, App Sequence 117, App Sequence 36, App1 Sequence 36, App1 Sequence 76, App1 Sequence 76, App1 Sequence 95, App1 Sequence 96, App1 Sequence 43, App1 Sequence 46, App1 Sequence 57, App1 Sequence 58, App1 Sequence 58, App1 Sequence 58, App1 Sequence 57, App1 Sequence 176, App Sequence 176, App1 Sequence 10, App1 Sequence 10, App1 Sequence 2, App1 Sequence 3, App1 Sequence 2, App1 Sequence 2, App1 Sequence 2, App1 Sequence 3, App1 Sequence 2, App1 Sequence 3, App1 Sequence 3, App1 Sequence 3, App1 Sequence 4, App1 Sequ

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Sequence 2, Application US/10044569B
; Sequence 2, Application US/20015268A1
; Deblication No. US203030175268A1
; GENERAL INFORMATION:
    APPLICANT: D. Collen Research Foundation vzw
    APPLICANT: Jacquemin, Marc G
    APPLICANT: Saint-Remy, Jean-Marie R
    TITLE OF INVENTION: Method and pharmaceutical composition for preventing
    TITLE OF INVENTION: Method and pharmaceutical composition for preventing
    TITLE OF INVENTION: Method and pharmaceutical composition for preventing
    TITLE OF INVENTION: Method and pharmaceutical composition for preventing
    TITLE OF INVENTION NUMBER: US,002-01-11
    PRIOR PLILING DATE: 2002-01-11
    PRIOR FILING DATE: 2001-01-11
    PRIOR FILING DATE: 2001-01-11
    SOFTWARE: Patentin Version 3.1
    SEQ ID NOS: 8
    SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature

; LOCATION: (343)...(375)

; OTHER INFORMATION: complementary determining region number three

US-10-044-569B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (130)...(159)
OTHER INFORMATION: complementary determining region number one FEATURE:
NAME/KEY: misc feature
LOCATION: (202)...(258)
OTHER INFORMATION: complementary determining region number two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 788; DB 14; Best Local Similarity 100.0%; Pred. No. 4.5e-63; Matches 150; Conservative 0; Mismatches 0;
4 US-10-384-933-157
4 US-10-216-484-117
5 US-10-264-049-4263
6 US-09-825-012-66
6 US-09-825-012-80
0 US-09-825-012-82
0 US-09-825-012-83
0 US-10-047-542-45
0 US-10-047-542-45
0 US-10-047-542-43
0 US-10-047-542-43
0 US-10-047-542-43
0 US-10-047-542-43
0 US-10-047-542-43
0 US-10-047-542-43
0 US-10-047-543-43
0 US-10-085-23A-10
2 US-10-389-223A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
   LENGTH: 150
    Sequence 2, Appli
Sequence 12, Appl
Sequence 10, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 14, Appl
Sequence 143, Appli
Sequence 143, Appl
Sequence 147, Appl
Sequence 145, Appl
Sequence 145, Appl
Sequence 145, Appl
Sequence 145, Appl
                                                                                                      April 5, 2004, 13:42:12; Search time 35.2792 Seconds (without alignments) 1116.513 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                   US-10-044-569B-2
788
1 MDWTWRILFLVAAATGTHAQ.......MVTVSSASTKGPSVFPLGSR 150
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| Cgn2 | Cyptodata | Z/pubpaa/US07 PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOF NEW PUB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOF NEW PUB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOF PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | DEGOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | DEGOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
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| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
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| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
| Cgn2 | Cyptodata | Z/pubpaa | USOB | PUBCOMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-390-986-12
US-09-747-669-3
US-09-747-669-3
US-10-225-108A-16
US-10-225-108A-16
US-10-216-484-143
US-10-216-484-143
US-10-384-933-143
US-10-384-933-143
US-10-384-933-145
US-10-384-933-145
US-10-216-484-145
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                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*
                                                                              - protein search, using sw model
                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Match Length DB
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Perfect score:
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                                                                                                         Run on:
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Length 150; Indels

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Sequence 28, Application US/09859053

Sequence 28, Application US/09859053

Patent No. US2020102658A1

GENERAL INFORMATION:

APPLICANT: Tauli, Takashi

APPLICANT: Tauli, Takashi

APPLICANT: Tauli, Takashi

APPLICANT: Tauli, Takashi

APPLICANT: HOUND US202012658A1uaki

APPLICANT: HOUND US202012658A1uaki

APPLICANT: HOUND US202012658A1uaki

TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND

TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND

FILE REFERENCE: 06501-07901

CURRENT APPLICATION NUMBER: US/09/859,053

CURRENT APPLICATION NUMBER: US/09/859,063

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2000-06-18

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 470

MUMBER 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GKGLEWMGSFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLKSEDTAVYYCATSTV 120
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74.9%; Score 590; DB 9; Length 47
Best Local Similarity 75.5%; Pred. No. 9.4e-45;
Matches 117; Conservative 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                              DB 14;
                                                                                                                                                                                                      Score 625.5; DB 14;
Pred. No. 1.7e-48;
7; Mismatches 13;
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                                                                                                                                                                                                         Query Match
Best Local Similarity 84.2%;
Matches 123; Conservative 7
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 146
                                                                                                   TYPE: PRT
CAGANISM: Homo sapiens
US-10-390-986-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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US-09-747-669-3
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Sublication No. US20030166011A1
GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: and Medicinal Uses Thereof
FILE OF INVENTION: and Medicinal Uses Thereof
FILE REPERBNCE: J1-009PCT
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/10/390,986
PRIOR APPLICATION NUMBER: US/99/582,337
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 1997-12-25
PRIOR PILING DATE: 1997-12-25
PRIOR APPLICATION NUMBER: JP P1998-356183
PRIOR FILING DATE: 1998-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor TITLE OF INVENTION: and Medicinal Uses Thereof
FILE REPERENCE: J1-009PCT
CURRENT APPLICATION NUMBER: U3/10/390,986
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: U5/95/82,337
PRIOR APPLICATION NUMBER: U5/95/82,337
PRIOR FILING DATE: 1997-12-25
PRIOR FILING DATE: 1997-12-25
PRIOR FILING DATE: 1997-12-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
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                               9
                                                                               1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.6%; Score 627.5; DB 14; Length Best Local Similarity 84.2%; Pred. No. 1.1e-48; Matches 123; Conservative 7; Mismatches 13; Indels
                                                                                                                                                                                                                                           121 DAFDIWGQGTMVTVSSASTKGPSVFPLGSR 150
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                                                                                                                                                                                                                                                                                                                                                                                              US-10-390-986-12
Sequence 12, Application US/10390986
Publication No. US20030166011A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CAGANISM: Homo sapiens
US-10-390-986-12
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US-10-390-986-10
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LENGTH: 146
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61 GKGLEWVGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYC----
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| Publication No. US2004001367241
| GENERAL INFORMATION:
| APPLICANT: Dietzschold, Bernhard
| APPLICANT: Dietzschold, Bernhard
| APPLICANT: Hooper, Douglas C.
| APPLICANT: Hooper, Douglas C.
| ATILE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
| TITLE OF INVENTION: AND METHODS FOR NAKING AND USING THE SAME
| TITLE OF INVENTION: 2013-140C11-185685
| CURRENT APPLICATION NUMBER: US/10/461,148
| CURRENT FILING DATE: 2003-06-13
| PRIOR FILING DATE: 2003-08-21
| PRIOR PRILING DATE: 2001-08-21
| PRIOR APPLICATION NUMBER: US 60/314,023
| PRIOR FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rubitaction No. USZUUJOLS/11ZA1
GENERAL INFORMATION:
APPLICANT: HOOPER, Craig
APPLICANT: DIETZSCHOLD, Bernhard
TITLE OF INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: and Methods for Making Them
FILE REFERENCE: 8321-110
CURRENT APPLICATION NUMBER: US 09/848,832
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-05-16
SPRIOR FILING DATE: 2001-08-16
SPRIOR FILING DATE: 2001-08-16
SOFTWARE: FastSEQ for Windows Version 4.0
SSO ID NO 16
TEMBER OF SEC ID NOS: 16
SSO ID NO 16
TEMBER OF SEC ID NOS: 16
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                                                                                                                                                                                                                                                              116 ----AVPDPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                 121 NVEMAÁIYHYYGMDVWGÓGTTVTVSSÁSTKGÞSVFÞL 157
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67.5%; Score 532; DB 14;
Best Local Similarity 67.5%; Pred. No. 1.5e-39;
Matches 106; Conservative 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/10225108A Publication No. US20030157112A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-225-108A-16
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APPLICANT: Dan, Michael D.
APPLICANT: Dan, Michael D.
APPLICANT: Saleh, Mansoor
TITLE OF INVENTION: 485, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLECTIBES
TITLE OF INVENTION: ENCODING THE FRACHENTS, AND USE THEREOF FOR THE PROPHYLAXIS
TITLE OF INVENTION: ENCODING THE FRACHENTS, AND USE THEREOF FOR THE PROPHYLAXIS
TITLE OF INVENTION: ENCODING THE FRACHENTS, AND USE THEREOF FOR THE PROPHYLAXIS
TITLE OF INVENTION: AND DETECTION OF CANCERS
FILE REPERENCE: 3002-11-08
FILE REPERENCE: 3002-11-08
FILE REPERENCE: 1000-12-21
FRICK APPLICATION NUMBER: US 09/747,669
FRICK APPLICATION NUMBER: US 09/711,286
FRICK APPLICATION NUMBER: US 09/711,286
FRICK APPLICATION NUMBER: US 09/111,286
FRICK APPLICATION NUMBER: US 09/111,286
FRICK APPLICATION NUMBER: US 06/051,945
FRICK FILING DATE: 1998-07-07
FRICK FILING DATE: 1998-07-07-08
FRICK FI
                                       61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYC---- 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.4%; Score 539; DB 9; Best Local Similarity 66.9%; Pred. No. 3.6e-40; Matches 105; Conservative 16; Mismatches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic construct US-09-747-669-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/10290703
Publication No. US20030118593A1
GENERAL INFORMATION:
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           APPLICANT: Dan, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 105; Conserv
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                                                                                                                                                                                                                                                                                                                              1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTBLPVHWVGQAP 60
                                                                                                                                                                                                                                                                                                                                                                        1 MDWIWRFLFVVAAAIGVQSQVQLVQSGAEVKKPGSSVKVSCKASGGIFNRYIVNWVRQAP 60
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                                                                                                                                                                                                                                                                                    Indels 10;
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                                                                                                                                                                                                                                       Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DNSGTYYYFSGWFDPWGQGTLVTVSSASTKGPSVFPL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DA------FDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                  Query Match 67.5%; Score 532; DB 15; Best Local Similarity 67.5%; Pred. No. 1.5e-39; Matches 106; Conservative 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haruyama, No. US20030103976Alufusa APPLICANT: Haruyama, Hideyuki APPLICANT: Haruyama, Hideyuki APPLICANT: Haruyama, Hideyuki APPLICANT: Tamaki, Ikuko APPLICANT: Tamaki, Ikuko ITLE REPERENCE: 980126CIP/HG CURRENT PELROANTION NUMBER: US/09/499,662 PRIOR PELICATION NUMBER: US/09/499,662 PRIOR APPLICATION NUMBER: US/09/499,662 PRIOR APPLICATION NUMBER: US/09/499,662 PRIOR PILING DATE: 2000-02-09 PRIOR PELING DATE: 1998-04-01 NUMBER: US/09/499,662 PRIOR PELING DATE: 1998-04-01 PRIOR FILING DATE: 1998-04-01 SEQ ID NO 143
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PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 143, Application US/10216484 Publication No. US20030103976A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                        TYPE: PRT

CRGANISM: Human
US-10-461-148-9
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US-10-216-484-143
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RESULT 10

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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCA--- 116
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| Publication No. US2003170817A1
| Sequence 143, Application No. US2003170817A1
| APPLICANT: Serizawa, No. US20030170817A1ufusa
| APPLICANT: Serizawa, No. US20030170817A1ufusa
| APPLICANT: Makahara, Kaori
| APPLICANT: Tamaki, Ikuko
| TITLE OF INVENTION: Anti-Fas Anti-Fas Anti-Fas AppliCANT: Tamaki, Ikuko
| TITLE REPERENCE: 980126CIP/HG
| CURRENT APPLICATION NUMBER: US/09/499,662
| PRIOR APPLICATION NUMBER: US/09/499,662
| PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 09/053,583
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
| NUMBER OF SEQ ID NOS: 165
| TENCHMENT OF SEQ ID NOS: 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Designed heavy OTHER INFORMATION: chain of humanized anti-Fas antibody
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66.6%; Score 525; DB 14;
Best Local Similarity 68.2%; Pred. No. 6.3e-39;
Matches 103; Conservative 14; Mismatches 30;
                                                                             APPLICANT: BARANARA, NO. US20030103976Alufusa APPLICANT: Haruyama, Hideyuki APPLICANT: Nakahara, Kaori APPLICANT: Nakahara, Kaori APPLICANT: Tamaki, Ikuko APPLICANT: Tamaki, Ikuko APPLICANT: Tamahashi, Tohru TITE OF INVENTION: ANLI-FRA Antibodies FILE REPRENCE: 980126CTP/HG CURRENT APPLICATION NUMBER: US/10/216,484; CURRENT FILING DATE: 2002-09-09 PRIOR APPLICATION NUMBER: US 09/053,583 PRIOR FILING DATE: 2000-02-09 PRIOR FILING DATE: 1998-04-01 NUMBER OF SEQ ID NOS: 165
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Sequence 147, Application US/10216484 Publication No. US20030103976A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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) OTHER INFORMAT
US-10-384-933-145
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                                                                                                                                                                 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA---- 116
                                                                                                                                                                                             61 GCGLEHWGEIDPSDSYINYNQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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APPLICANT: Berizawa, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
IKUKATI Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
ITILE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 960126CIP/HG
CURRENT APPLICATION NUMBER: US/03/499,662
PRIOR APPLICATION NUMBER: US/03/499,662
PRIOR FILING DATE: 2000-02-05
PRIOR FILING DATE: EARLIER PLING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 147
                                                                  1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                   1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.6%; Score 525; DB 14; Length 470; 68.2%; Pred. No. 6.3e-39; tive 14; Mismatches 30; Indels
                         Indels
  Best Local Similarity 68.2%; Pred. No. 6.3e-39;
Matches 103; Conservative 14; Mismatches 30;
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APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakabara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Tohru
APPLICANT: Takababhi, Tohru
TILE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
Pred. No.
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Publication No. US20030170817A1
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Best Local Similarity 68.2%
Matches 103; Conservative
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US-10-216-484-145
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCA---- 116
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Sequence 145, Application US/10384933

Publication No. US20030170817A1

SEMERAL INFORMATION:
APPLICANT: Barizawa, No. US20030170817Alufusa

APPLICANT: Tawahashi, Tohru

APPLICANT: Tawahashi, Tohru

APPLICANT: Tawahashi, Tohru

APPLICANT: Tawahashi, Tohru

TITLE OF INVENTION: Anti- Fas Antibodies

FILE REFERENCE: 380126C1P/HG

CURRENT APPLICATION NUMBER: US/10/384,933

CURRENT APPLICATION NUMBER: US/10/489,662

PRIOR FILING DATE: 2000-02-09

PRIOR PILING DATE: EARLIER RAPLICATION NUMBER: BARLIER APPLICATION NUMBER: 1998-04-01

NUMBER OF SEQ ID NOS: 165

SEQ ID NO 145

TAWATHA. APPLICATION NUMBER: 1508-04-01
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Best Local Similarity 68.2%; Pred. No. 7.8e-39;
Matches 103; Conservative 14; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.5%; Score 524; DB 14; Best Local Similarity 68.2%; Pred. No. 7.8e-39; Matches 103; Conservative 14; Mismatches 30;
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CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER: OF SEQ ID NOS: 165
SEQ ID NO 145
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ORGANISM: Artificial Sequence
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA---- 116
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OTHER INFORMATION: Description of Artificial Sequence: Designed
OTHER INFORMATION: heavy chain of humanized anti-Fas antibody
US-10-216-484-157
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                                                                                                                                                       Sequence 157, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Tohru
GURRENT PAPLICATION NUMBER: US/10/216,484
CURRENT APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 1908-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 157
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                              TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-216-484-157
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April 5, 2004, 13:36:42 ; Search time 13.4518 Seconds (without alignments) 575.678 Million cell updates/sec
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1 MDWTWRILFLVAAATGTHAQ.......MVTVSSASTKGPSVFPLGSR 150
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1: /ogn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 12, Appl Sequence 10, Appl Sequence 110, Appl Sequence 13, Appl Sequence 13, Appl Sequence 45, Appl Sequence 41, Appl Sequence 10, Appl Sequence 102, Appl Sequence 102, Appl Sequence 102, Appl Sequence 100, Appl Sequence 141, Appl S Sequence 7, Appli Sequence 8, Appli Sequence 8, Appli Sequence 112, App Sequence 99, Appli Sequence 99, Appli Sequence 90, Appli Sequence 4, Appli Sequence 17, Appli Sequence 17, Appli Description SUMMARIES Query Match Length DB Score Result No.

58.6 142 5 PCT-U595-01219-17 Sequence 17, Appl 58.8 135 1 US-O8-4-778-19 Sequence 19, Appl 58.8 135 1 US-O8-477-728-19 Sequence 19, Appl 58.8 135 1 US-O8-477-040-19 Sequence 19, Appl 58.8 135 1 US-O8-477-040-19 Sequence 19, Appl 58.8 135 2 US-O8-5698-31 Sequence 19, Appl 58.8 135 2 US-O8-579-3784-12 Sequence 11, Appl 58.8 140 3 US-O8-579-3784-12 Sequence 12, Appl 58.8 140 5 PCT-US33-11612-12 Sequence 12, Appl 58.7 139 1 US-O8-452-164A-19 Sequence 19, Appl 58.7 139 2 US-O8-452-164A-19 Sequence 19, Appl 58.7 139 4 US-O8-452-164A-19 Sequence 19, Appl 58.7 139 4 US-O8-476-176B-14 Sequence 14, Appl 58.6 142 2 US-O8-476-176B-14 Sequence 14, Appl 58.6 142 3 US-O8-85-66-63 Sequence 14, Appl 58.4 140 3 US-O8-85-61-63 Sequence 63, Appl 58.4 140 4 US-O8-436-561-63 Sequence 63, Appl	RESULT 1 US-09-582-337-12 US-09-582-337-12 Sequence 12, Application US/09582337 Sequence 12, Application US/09582337 Sequence 12, Application US/09582337 Sequence 12, Application US/09582337 SEQUENCE INFORMATION: APPLICATION: APPLICATION: MONOCIONAL Antibody Against Connective Tissue Growth Factor TITLE OF INVENTION: and Medicinal USes Thereof TITLE OF INVENTION: MONOCIONAL ANTIBORY FILING DATE: 10997-12-23 PRIOR FILING DATE: 1997-12-25 PRIOR FILING DATE: 1997-12-15 PRIOR FILING DATE: 1997-12-15 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin Ver: 2.0 SOFTWARE: Patentin Ver: 2.0 SOFTWARE: PATENTIAL ANTIBORY TYPE: RT CORGANISM: Homo sapiens	imilarity 84.2%; Score 627.5; DB 4; Length 146; imilarity 84.2%; Pred. No. 4.2e-51; Conservative 7; Mismatches 13; Indels 3; Gaps 1; Conservative 7; Mismatches 13; Indels 3; Gaps 1; MDMTWRILELVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60 MDCTWRIPFLVAAATGTHAQVQLVQSGAEVKRPGASVKVSCKVSGYTLTELPVHWVGAP 60 GKGLEWVGSFDPESGESIYAREFOGSVTMTADISTDIAYMELSSLRSDDTAVYYCAV 117 GKGLEWWGSFDPEDGETIYAQKFQGRVTMTEDTSTDIAYMELSSLRSEDTAVYYCAV 117 GKGLEWMGSFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATSTV 120 PDPDAFDIMGQGTMVTVSSASTKGPS 143 I	IS-SULT 2 Sequence 10, Application US/09582337 Sequence 10, Application US/09582337 Sequence 10, Application US/09582337 Sequence 10, Application US/09582337 GENERAL INFORMATION: APPLICANT: Japan Tobacco, Inc. TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor TITLE OF INVENTION: and Medicinal Uses Thereof FILE REFERENCE: J1-099PCT CURRENT APPLICATION NUMBER: US/09/582,337
	Applica Applica 5:62618 8:62618 Applica Japan To VENTION:	imilarity i Conserv MDWTWRILFL MDCTWRIFFL GKGLEWWGSF GKGLEWMGSF CYGLEWMGSF	-10 , Applica 6562618 ORMATION: Japan TO NVENTION: NVENTION: ENCE: J1-
444444 4444 000000 000 000 4 W W W W W W W W W W W W W W W W W W W	TLT 1 9-582-337-: quence 12, quence 12, quence 12, ILLE EFFERBITLE OF INV ITLE OF INV ITLE REFERBITLE OF INV RENT APPLITURENT	Match Natch Socal S es 123 es 121 es 12 es	2 - 337-10 Aprint No. 6562 int No. 6562 RAL INFORMATION INTERNATION INTERNATIO
GOUNUUUUUUUUUUUAAAAAA 8001101440010001011440	RESULT US-09-1- Seque Result APPRIL TITIT TITIT PRIL PRIL SOOF	Db Db Oye Db Oy	RESULT US-60- S-60- Pate GENE TIT FILL

us-10-044-569b-2.rai

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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-08-545-809A-110

| Sequence 110, Application US/08545809A
| Patent No: 6096878
| GENERAL INFORMATION:
| APPLICANT: Hord/o, Tasuku
| APPLICANT: Hord/o, Tasuku
| TITLE OF INVENTION: Fuminiko
| TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
| NUMBER OF SEQUENCES: 145
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Fish & Richardson, P.C.
| STREET: 225 Franklin Street
| CITY: Roston
                                                                                                                                                                                                                                                                                                                                                                                             1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                  Length 467;
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                                                                                                                                                                                                                                                                                                                                      20, Indels
                                                                                                                                                                                                                                                                               71.5%; Score 563.5; DB 3; 73.0%; Pred. No. 1.4e-44; iive 19; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: MA
COUNTRY: MA
CONTRY: MS
ZIP: 02110-2804
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows Version 2.0
CURRENT APPLICATION UNDER: US/08/545,809A
FILING DATE: 27-MAR-1996
FRIOR APPLICATION NUMBER: PCT/JD93/00603
FILING DATE: 10-MAY-1933
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
RESISTRATION NUMBER: 29,066
RESISTRATION NUMBER: 29,066
RESISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECHANNICATION INFORMATION:
TELECHANNICATION:
TELECHANNICATION INFORMATION:
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Pred. No. 1.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DFFFDFWGQGTMVTVSSASTKGPSVFPL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 D-AFDIWGQGTMVTVSSASTKGPSVFPL 147
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
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87.9%;
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amino acid
                                 467 amino acids
                                                   TYPE: amino acid
STRANDENESS: single
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTUT11
CLONE: 2747531
US-09-049-672A-8
                                                                                                                                                                                                                                                                                                                                         Conservative
   SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 108; Conserv
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Best Local Similarity
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                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Sequence 8 Application US/09049672A;
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Yu-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1074'F PATER Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                  ж
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                           Query Match
79.4%; Score 625.5; DB 4
Best Local Similarity 84.2%; Pred. No. 6.4e-51;
Matches 123; Conservative 7; Mismatches 13
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: JP P1997-367699
PRIOR FILING DATE: 1997-12-25
PRIOR APPLICATION NUMBER: JP P1998-356183
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 PDPDAFDIWGQGTMVTVSSASTKGPS 143
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REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650-845-4166
                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-09-582-337-10
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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US-09-049-672A-8
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCAVP-D 119
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC COMPATIBLE
COMPUTER: DE PC COMPATIBLE
COMPATER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,968
FILING DATE: 11-SEP-1995
CLASSIFICATION NUMBER: US/08/513,968
FILING DATE: 11-MAR-1993
ATTONNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: ES,618
REFERENCE/DOCKET NUMBER: ES,618
REFERENCE/DOCKET NUMBER: ES,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-HIV MONOCLONAL ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.2%; Score 513.5; DB 3 69.3%; Pred. No. 1.5e-40; tive 16; Mismatches 25
                                                             118 PDPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                         Sequence 38, Application US/08513968
Patent No. 6114143
                                                                                                                                                                                                                                                                                                                                           APPLICANT: CSATOMI, KIYOSHI APPLICANT: KTMACHI, KAZULIKO APPLICANT: HIGUCHI, HICÉUMI APPLICANT: TOKIYOSHI, SACOHIO TITLE OF INVENTION: ANTI-HIV MC NUMBER OF SEQUENCES: 86 CORRESPONDENCE ADDESSS: ADDESSES: BROWDY AND NEIMARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 PDAFDIWGQGTMVTVSS 136
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                                                                                                                                                                                                                                                                                                                                  SHIOSAKI, Kouichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 137 amil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 137 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFHONE: 202-628-5197
TELEFAX: 202-737-3528
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Best Local Similarity
Matches 95; Conserva
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                            1 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAP 60
                                                                                                                      61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA 116
                                                                                                                                              61 GKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCA 116
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  Gaps
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APPLICANT: Yue, Henry
APPLICANT: Yue, Venry
APPLICANT: Corley, Noil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: SYSTEM ASSOCIATED PROTEINS NUMBER OF SEQUENCES: 28
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  8; Indels
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; Pred. No. 4e-41;
16; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIALE
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                Sequence 13, Application US/09049672A
Patent No. 6135941
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9
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CLASSIFICATION: 536
PRIOR APPLICATION 536
PRIOR APPLICATION DATE:
PILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: CETTONE, MICHAEL C
REGISTRATION NUMBER: 39,132
REPERCE/DOCKET VUMBER: PF-
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                  Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 67.3%;
Matches 101; Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX:
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                 Lal, Preeti
Tang, Y. Tom
Yue, Henry
  102; Conservative
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TELEFAX: 650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LIBRARY: SYNON
; CLONE: 3551457
US-09-049-672A-13
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Matches
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61 GQGLEWMGGIIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDTAVYYCAT--- 117
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Patent No. 6455677
Patent No. 645677
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                      Patent No. 5875961
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: MASHINGTON
STATE: D. C.
COUNTRY: U.S.
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4.7e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNOT, BARBARA G
REGISTARION NUMBER: 30,377
REPERRICE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 10, Application US/08378939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
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amino acid
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Best Local Similarity 62.5%
Matches 100; Conservative
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MOLECULE TYPE: protein
US-08-378-939-10
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-301-593-43
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                                                                                                                                                                    APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARCARET D.
ADDRESSES: ALLEGREFITT C. MATTER THENT OF AIDS, ARC AND HIV INFECTION NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS: ALLEGREFITT C. MATTER ADDRESSES: ALLEGREFITT C. MATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: ALLGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 66.66
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION ADAR:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: O7/618,542
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
APPLICATION NUMBER: 26,949
RESTERENCE/DOCKET NUMBER: 26,949
TELECOMMUNICATION INFORMATION:
TELEFRAX: (312) 715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
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                                                                                                                                                               Sequence 45, Application US/07916098A
Patent No. 5871732
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAN: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 467 amino acids
amino acid
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Best Local Similarity 64.5*
Matches 98, Conservative
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RESULT 8 US-08-378-939-10

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                                                                                                                                                                                                                                                                         Query Match 63.8%; Score 503; DB 4; Length 472; Best Local Similarity 63.6%; Pred. No. 5.7e-39; Matches 98; Conservative 15; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bendig, Mary M.
APPLICANT: Bendig, Mary M.
APPLICANT: Kettleborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

WEDIUM TYPE: RIADABLE FORM:

MEDIUM TYPE: ROOMPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: PATENTO BATE: 06-NOV-1992

FILING DATE: 06-NOV-1992

CLASSIFICATION NUMBER: WO PCT/EP92/00480

PRIOR APPLICATION NUMBER: BP 911933892

PRIOR APPLICATION NUMBER: BP 911933892

ATTORNEY/AGBNT INFORMATION:
NAMME: Hamlet-King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/POCKET NUMBER: Merck 1430

TELECOMMUNICATION NUMBER: Merck 1430

TELECOMMUNICATION NUMBER: Merck 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Millen, White, Zelano & Branigan,
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 ---VPDPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AYGYDEGHAMDYWGQGTLVTVSS-STKGPSVFPL 153
EARLIER APPLICATION NUMBER: BP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.0
EEQ ID NO 43
LENGTH: 472
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Patent No. 5558864
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 140 amino acids
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                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo, sapiens
US-09-301-593-43
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US-09-982-337-8

| Sequence 8, Application US/09582337 |
| Patent No. 65218 |
| General No. 65218 |
| TITLE OF INVENTION: And Medicinal Antibody Against Connective Tissue Growth Factor |
| TITLE OF INVENTION: and Medicinal Uses Thereof |
| TITLE OF INVENTION: and Medicinal Uses Thereof |
| FILE REPRENCE: J1-009CT |
| CURRENT FILING DATE: 2000-06-23 |
| PRIOR APPLICATION NUMBER: JP P1997-367699 |
| PRIOR APPLICATION NUMBER: JP P1998-356183 |
| NUMBER OF SEQ ID NOS: 27 |
| SEQ ID NO 8 |
| SEQ ID NO 9 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 WVRQAPGOGLEWMGWINPNSSGTHYAQMFQGRVTVTRDTSISTAYMELSRLRSDDTAVYY 115
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                                                                                                                                                                                                                                                                                                                                                              1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSSHWMHWVRQAP
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                                                                                                                                                                       Length 140;
                                                                                                                                                                                                                                                                          26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 102, Application US/08137117D
Patent NO. 5795965
GENERAL INFORMATION:
APPLICANT: STOCK KAN
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
                                                                                                                                                                                 63.6%; Score 501; DB 1;
68.6%; Pred. No. 2.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 496; DB 4;
Pred. No. 6.9e-39;
9; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 CAVPDPDA----FDIWGQGTMVTVSSASTKGPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 CAREGIAAAIYGMDVWGQGTTVTVSSASTKGPS 149
                                                                                                                                                                                                                                                                14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 D----AFDIWGQGTMVTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.9%;
                                                                                                                                                                            Query Match
Best Local Similarity 68.6%
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.99
Matches 103; Conservative
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CORGANISM: Homo sapiens
US-09-582-337-8
; TYPE: amino acid
; TOPOLOGY: linear
US-07-946-421-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-137-117D-102
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELFVHWVGQAP
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US-08-649-100-41
US-08-649-100-41
| Sequence 41, Application US/08649100 |
| Patent No. 6114507 |
| GENERAL INFORMATION: |
| APPLICANT: SHIRATAWA, KAMON |
| APPLICANT: NAGATA, SHIGEKAZU |
| TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY |
| TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY |
| NUMBER OF SEQUENCES: 41 |
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                           COMPUTER: IEM PC COMPATIONS
COPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE: US/08/436,717
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US/08/137,117
FILING DATE: 24-APR-1992
APPLICATION NUMBER: W PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: W P-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/15
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: US/08/15
FILING DATE: 25-APR-1991
ATPORNEY/AGENT INFORMATION:
NAME: WEGNER, HAZOIG C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 25,258
REFERENCE/OFFICE NUMBER: COLD/GT-25,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches
                        , Suite 500
                                                                                                  COMPLEX: CONT-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DAFDIWGOGTMVTVSS 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-436-717-102
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Best Local Similarity
Matches 93; Conserva
                                         Washington
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  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 135;
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Patent No. 5817790

GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: SALDAWHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: U6/08/137,117D
FILING DATE: 24-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: U6/08/24
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 24-APR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: J9-FBB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: J9-FBB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 25,258
FILING DATE: 25-APR-1991
ATFORNEY/AGENT INFORMATION:
NAME: MEGNER, Harold C.

REGISTRATION NUMBER: 25,258
REFERRICE/DOCKET NUMBER: 25,258
REFERRICE/OMCHINICATION INFORMATION:
TELEFPAX: (202) 672-5309
THELEFFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.5%; Score 492.5; DB 1;
68.4%; Pred. No. 1.3e-38;
tive 16; Mismatches 26;
                                                                  ., Suite 500
                                                                                                                                                   ZIP: 20007-5109
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELBEAK: (202, CTELEFAK: (202, CTELEK: 90415
TELEX: 90415
INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS: LENGTH: 135 amino acids TVPE: amino acids Tinear
                                            3: Foley & Lardner
3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DAFDIWGQGTMVTVSS 136
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120 NRFAYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 68.48
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / MOLECULE TYPE: protein US-08-137-117D-102
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & La
STREET: 3000 K Street
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-08-436-717-102
                                                                                   CITY: Was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDWVWTLLFLIAAAQSAQAQVQLVQSGAEVKKPGSSVKVSCKASGYTFTEYPMHWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 100, Application US/08137117D
Fatent No. 2795965
Fatent No. 2795965
GENERAL INFORMATION:
APPLICANT: TSUCHIXA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: SALDAHA, Jose
APPLICANT: SALDAHA, Jose
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRES:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                  SOFTWARE PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WORREY OR, GERALD M
REGISTRATION NUMBER: 28,977
REGISTRATION NUMBER: 1110-160
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.4%; Score 492; Best Local Similarity 68.4%; Pred. No. 1 Matches 93; Conservative 13; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: PatentIn Release #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DAFDIWGQGTMVTVSS 136
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                                                                                                     ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
OPERATING SYSTEM: PC-DOS/M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 136 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-08-649-100-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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61 GQGLEWVGYIDPFNGGTSYNQKFKGKVTMTVDTSTWTAYMELSSLRSEDTACYYCA-RGG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.0%; Score 488.5; DB 1; Length 135; 68.4%; Pred. No. 3.1e-38;
APPLICATION NOMBER: US/08/13/,11/D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATE: WOOF PROPERTY PAPEL PAPEL PROPERTY PAPEL PROPERTY PAPEL PRIOR APPLICATION NUMBER: WOOF PAPEL PAPEL PROPERTY PAPEL PAPEL PROPERTY PAPEL P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEXA: (202/0...
TELEXA: 904136
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
SEQUENCE: amino acids
"VPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DAFDIWGOGTMVTVSS 136
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Best Local Similarity 68.43
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE
US-08-137-117D-100
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chain pre chain V r chain V-J chain - h

chain chain chain

chain

kappa kappa

chain chain chain

chain

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S49534
autibody VL chain (V kappa 3/J kappa 2) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: S49532
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Reference number: S48797
A;Reference number: S48797
A;Reference number: S48797
A;Reference: L129 cMBH>
A;Residues: 1-129 cMBH>
A;Residues: 1-129 cMBH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYXCQQYGSSPQTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Askpedies: Homo angless (man)
C;Species: Homo appless (man)
C;Species: Homo sapiens (man)
C;Date: 20-Peb-1995 #sequence_revision 20-Peb-1995 #text_change 21-Jan-2000
C;Accession: S20631
A;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
Submitted to the EMBL Data Library, April 1992
A;Reference number: S20631
A;Accession: S20631
A;Status: preliminary
A;Anolecule rype: mRNA
A;Residues: 1-145 <LEB
A;Residues: 1-145 <LEB
A;Cross-references: EMBL:211903; NID:G33156; PIDN:CAA77955.1; PID:G33157
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
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85.9%; Score 630; DB 2; Length 129;
Best Local Similarity 94.5%; Fred. No. 4.7e-43;
Matches 121; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                              ALIGNMENTS
        $40344
C30608
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Ig kappa chain - h
                                                                  5, 2004, 13:25:01; Search time 11.533 Seconds (without alignments) 1184.358 Million cell updates/sec
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                                                                                                        US-10-044-569B-4
733
1 METPAQLLFLLLMLPDTTG.....TRLEIKGTVAAPSVPIFPPS 142
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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A years: Userlands: GDB:136266
A; Map position: 2p12-2p11
A; Complexe: An immunoglobulin heterotetramer subunit consists of two identical light (ka complexe: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into 1 C; Superfamily: immunoglobulin V region; immunoglobulin homology chronic 1ymphocytic leukemia, heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-117/Region: V segment
F;21-117/Region: V segment
F;35-111/Domain: immunoglobulin homology <IMM>
F;36-111/Domain: immunoglobulin homology <IMM>
F;36-111/Region: complementarity-determining 2
F;110-117/Region: complementarity-determining 3
F;110-117/Region: J segment (JKI)
F;31-109/Disulfide bonds: #status predicted
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Cybecies: O'-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
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C)Superfamily: immunoglobulin V region; immunoglobulin homology
C)Keywords: immunoglobulin
F)36-111/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.5e-42;
4; Mismatches 6; Indels
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                       J. EXP. Med. 167, 840-852, 1988
A;Title: Autcantibody-associated kappa light chain variable
A;Reference number: PL0021; MUID:88171307; PMID:3127527
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8.5e-42;
Chen, P.P.; Carson, D.A.
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83.8%; Score 614;
Best Local Similarity 92.2%; Pred. No. 8
Matches 118; Conservative 5; Mismatch
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C;Comment: The protein is one of
C;Genetics:
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Best Local Similarity 92.2
Matches 118; Conservative
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A.Map position: 2pi2-2pi1

C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la c; Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: autoantibody, chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;2-1129/Product: IG kappa chain V-III region (Hah) #status predicted <MAT>
F;2-111/Region: V segment
F;3-111/Domain: immunoglobulin homology <IMM>
F;4-55/Region: complementarity-determining 2
F;110-117/Region: complementarity-determining 3
F;110-117/Region: complementarity-determining 3
F;110-117/Region: J segment (JKI)
F;3-109/Disulfide bonds: #status predicted
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A,Residues: 1-129 <KIP>
C,Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
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C;Species: Homo sapiens (man)
C;pate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C;Accession: PLO021
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1.4e-42;
                                        DB 2;
                                 Score 627; DB 2,
Pred. No. 9e-43;
9; Mismatches 1
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4; Mismatches
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Best Local Similarity 93.8%;
Matches 120; Conservative
                                        85.5%;
          Query Match
Pest Local Similarity 83.0.
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QGTKVEIK 128
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120
                                                 60 PGQAPRILLIYDASNRATGIPARFSGSGTDFTLTISSLBPEDFAVYYCQQRSNWPLTFG 119
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                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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   PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG
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C'Species: Homo sapiens (man)
C'Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C'Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R'Klein, R.; Jaenichen, R.; Zachau, H.G.
R'Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A; Ritle: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: $40312; MUID:94080891; PMID:8258341
A; Accession: $40327
A; Atatus: preliminary; translation not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 36-111/Domain: immunoglobulin homology < IMM>
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C; Accession: $20636

Bridges, L.S.; Koopman, W.J.; Schroeder, H.W. submittee, C.Y.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W. submittee, C.Y.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W. A; Reference number: $20631

A; Reference number: $20636

A; Accession: $20636

A; Accession: $20636

A; Accession: $20636

A; Residues: 1-128 < LEE>
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82.9%; Score 608; DB 2; L
Best Local Similarity 91.4%; Pred. No. 2.5e-41;
Matches 117; Conservative 4; Mismatches 7;
                                                                                                                 142
                                                                                                                                                                     120 GGTKVEIKRTVAAPSVFIFPPS 141
                                                                                                                 121 OGTRLEIKGTVAAPSVFIFPPS
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Best Local Similarity 94.2%;
Matches 114; Conservative
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J. Exp. Med. 169, 1631-1643, 1989
A,Title: Relationship of variable region genes expressed by a human B cell lymphoma secr
A,Reference number: PL0106; MUID:89235583; PMID:2541221
                                                                                                                                                                                                                                                                                   C; Accession: 538643
R; Bensimon, C; Chastagner, P; Zouali, M.
submitted to the EMBL Data Library, November 1993
A; Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A; Reference number: 538643
A; Accession: 538643
A; Accession: 538643
A; Accession: 538643
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-134 < BEN>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < INM>
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0106
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A,Accession: PL0106
A,Molacule type: mRNA
A;Residues: 1-14 <SIL.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
C;Keywords: heteroterramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-115/Domain: immunoglobulin homology <IMM>F;21-115/Domain: immunoglobulin homology <IMM>F;44 54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;105-115/Region: complementarity-determining 3
F;116-1127/Domain: J region <JRG
F;128-144/Domain: C region (fragment) <CRE>
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Pred. No. 8.8e-42;
4; Mismatches 6; Indels
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ilarity 92.2%;
Conservative
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Best Local Similarity 85.2
Matches 121; Conservative
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                                                    QGTRLEIK 128
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Best Local Similarity
Matches 118; Conserv
            OGTRLEIK
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A;Residues: 1-116 <GRA>
A;Note: this sequence was translated from an aberrantly rearranged kappa gene from lamb
C;Genetics:
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                                                                               61 PGQAPRLLISGASRRATGIPDRFSGSGSGTDFTLTISRLEPEDFAMYYCQQYGSTPRTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 PRILIYGASTRATGIPDRFSGSGSTDFTLTISRLEPEDFAVYYCQKYGTSAITFGQGTR 124
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                                       PGOAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOKYGTSAITFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
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R.Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.

Bubmitted to the EMBL Data Library, April 1992.

A; Reference number: S20631

A; Accession: S20633

A; Accession: S20633

A; Accession: Preliminary

A; Status: preliminary

A; Residues: 1-124 <LEE>
A; Cross-references: EMBL: Z11891; NID: g33185; PIDN: CAA77945.1; PID: g33186

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: hetercterramer; immunoglobulin

F; 32-107/ Domain: immunoglobulin homology <IMM>
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A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>F;1-20/Domain: immunoglobulin homology <IVM>
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Best Local Similarity 95.73
Matches 110; Conservative
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 30-Sep-1991;#text_change 21-Jan-2000
C;Accession: A32274
C;Accession: A32274
B;Newkirk, M.M.; Gram, H.; Heinrich, G.F.; Oestberg, L.; Capra, J.D.; Wasserman, R.L.
J. Clin. Invest. 81, 1511-1518, 1988
A;Title: Complete protein sequences of the variable regions of the cloned heavy and ligh actors of the Wa idiotypic family.
A;Reference number: A92767; MUD:88213701; PMID:2452836
A;Accession: A32274
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A.Residues: 1-129 <NEW>
A.Cross-references GB:M20031
A.Note: the authors translated the codon GAT for residue 17 as Ala
A.Note: this sequence was determined from the differentiated gene
G.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Reywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence Hatatus predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region EVI-15 #status predicted <KV3>
F:36-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region - human C,Species: Homo sapiens (man)
C,Accession: S20637; S20632
R,Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
Submitted to the BMBL Data Library, April 1992
A,Reference number: S20637
A,Reference number: S20637
A,Reference number: S20637
A,Reference number: S20637
A,Residues: 1-130 <LEE>
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Pred. No. 5.6e-40;
7; Mismatches 7; Indels
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Best Local Similarity 89.1%;
Matches 114; Conservative
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Best Local Similarity 89.2%;
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS-AITFG 120
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1 METPAQLEILILMLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQK 60
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Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1999
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Accession: S40312; MUID:94080891; PMID:8258341
A;Accession: S40312; MUID:94080891; PMID:8258341
A;Accession: S40312
A;Accession: S40312
A;Accession: S40312
A;Accession: MANA
A;Residues: 1-129 <KIE>
A;Cross-references: EMBL:X72435; NID:9441338; PIDN:CAA51103.1; PID:9441339
C;Auperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-110/Domain: immunoglobulin homology <IMM>
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PO1617 PO1606 PO1603 PO1601 PP01610 PP01634 PO1634 PO1655 PO1665 PO1593

KV2D_HUMAN
KV1K_HUMAN
KV1I_HUMAN
KV1I_HUMAN
KV1R_HUMAN
KV4B_HUMAN
KV4B_MOUSE
KV3M_MOUSE

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5, 2004, 12:10:21 ; Search time 6.48731 Seconds (without alignments) 1139.758 Million cell updates/sec
                                                       US-10-044-569B-4
733
1 METPAQLLFLLLLMLPDTTG.....TRLBIKGTVAAPSVPIFPFS 142
    5.1.6
Compugen Ltd.
    GenCore version
Copyright (c) 1993 - 2004
                         protein search, using sw model
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Perfect score:
                         1
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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Length

Query Match

Score

Result No.

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

SwissProt_42:*

Database :

141681 segs, 52070155 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Sequence:

Description

homo sapien
mus musculu
homo sapien

KV31, HUMAN KV3M, HUMAN KV31, HUMAN KV31, HUMAN KV31, HUMAN KV32, HUMAN KV32, HUMAN KV32, HUMAN KV36, HUMAN KV36, HUMAN KV36, HUMAN KV37, HUMAN

HUMAN HUMAN MOUSE HUMAN

HUMAN HUMAN HUMAN

MOUSE

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PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120

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mus musculu homo sapien homo sapien homo sapien homo sapien

HUMAN HUMAN HUMAN

homo sapien homo sapien

METPAQLIFILLIMIPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQK 60

1 METPAQLLFLLLLWLPDTTGETALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK

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STANDARD;
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OGTKLEIK 127
                                                                                                                  Ig kappa chain V-III
Homo sapiens (Human)
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                              NCBI_TaxID=9606;
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Matches 111;
                  KV3K HUMAN
P06311;
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61 PGQAPRLLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Medicantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";

J. Exp. Med. 167:840-852(1988).

J. DISBASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.2e-52;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG KAPPA CHAIN V-III REGION HI FRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENORK-2.
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FRAMBWORK-3.
COMPLEMENTARITY-DETERMINING-3.
DXI. SEGNENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-III region HIC precursor.
Homo sapiens (Human)
                                                                                                                                                                                                 129 AA
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HSSP, PROJSZ, IWTL.
GO,GO:0005576; C:extracellular; NAS.
GO,GO:0003823; F:antigen binding; NAS.
GO,GO:0006955; P:immune response; NAS.
InterPro; IPRO07110; Ig-like.
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00047; ig; i. --
SMART, SM0406; IGv; i.
PROSITE, PS50835; IG LIKE; I.
Immunoglobulin V region; Signal.
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Best Local Similarity 92.2%;
Matches 118; Conservative 5
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QGTKVEIK 128
                                                            QGTRLEIK 128
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OGTKVEIK 128
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110
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129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                              KV3M HUMAN
P18136;
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NON TER
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RESULT 3

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PRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JXI SEGNENT.
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                                                  01-JAN-1988 (Rel. 06, Greated)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region IARC/BL41 precursor.
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86.7%; Pred. No. 3.6e-47;
ive 5; Mismatches 11
128 AA.
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PIR; A01899; K3HU41.
HSSP; PO1607; LRL
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; IQ-like.
InterPro; IPR00710; IQ-like.
InterPro; IPR00710; IQ-like.
INTERPRO; IPR00710; IQ-like.
INTERPRO; IPR0047; IG; IG.
PROSITE; PSS0835; IG.IKE; I.
IMMUNOGlobulin V region; Signal.
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PRT;
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ID KV3H HUMAN
AC P04207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METPAQLLFLLLLWLPDTTGELALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PGQAPRLLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQK 111
                                                                                                               SEQUENCE FROM N.A.
MEDLINE=85087932; PubMed=6440122;
Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated within the VX locus.",
Nucleic Acids Res. 12:9229-9236(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG KAPPA CHAIN V-III REGION VG. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
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PRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12575 MW; 2DE47CDA3A17D555 CRC64;
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13-AUG-1987 (Rel. 05, Last sequence update)
15-AUG-1999 (Rel. 38, Last annotation update)
19 Aappa ohain V-III region VH precursor (Fragment).
Homo sapiens (Human).
    chain V-III region VG precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.4%; Score 508.5; DB 1; 91.0%; Pred. No. 1.8e-42; ive 1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P80362, 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0008955; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X01668; -; NOT_ANNOTATED_CDS.
PIR; A01900; K3HUVG.
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MEDLINE=85087932; PubMed=6440122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 91.0
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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115
108
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SEQUENCE
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P04434;
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                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEAPAQLLFLLLWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQK 59
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                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=86177570; PubMed=3083417;
MEDLINE=86177570; PubMed=3083417;
MEDLINE=86177570; Curd J.G., Chen P.P.
Goldfien R., Carson D.A.;
"Cloning and sequence determination of a human rheumatoid factor
                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
20-WAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-lli region CLL precursor (Rheumatoid factor).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG KAPPA CHAIN V-III REGION CLL.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 537; DB 1; Length 129;
Pred. No. 3.6e-45;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING-3. JK1 SEGMENT.
                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, bureze
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14275 MW; 5C13B411BE60CC14 CRC64;
                                                                                                                                                                                                                                                                        light.chain gene.";
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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(Rel. 05, Last sequence update)
(Rel. 38, Last annotation update)
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003537; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00047; ig; i. SMARY; SM00406; IGv; i. SMARY; SM00406; IGv; i. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%;
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HSSP; P80362; 1WTL.
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129 1
129 AA;
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13-AUG-1987
15-JUL-1999
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P04433;
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NON TER
SEQUENCE
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KV3I HUMAN ID KV3I HI AC P04433; DT 13-AUG-DT 13-AUG-DT 15-JUL-

RESULT 5

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Biochemistry 20:5816-5822(1981).
-!- MISCELLANGOUS: THIS CHAIN WAS ISOLATED FROM AN ICM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
PIR, A01896; K3HUWL.
HSSP, P80362, WWIL.
GO, GO:0005576; C:extracellular; NAS.
GO, GO:0005576; C:extracellular; NAS.
GO, GO:000823; F:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-82046598; PubMed-6794615;
Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
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                                                                                                                                                                                                                                                                                                                                                                                  21 BIALTOSPGTLSLSPGERATLSCRASOSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIP
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
16 Kappa chain V-III region WOL.
Homo sapiens (Human).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalais Eutharyota; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DRFSGSGSGTDFTLTISRLEPDDFAVYCQQYGSSPQTFGQGSKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOKYGTSAITFGQGTRLEIK 128
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                                                                                                                                                                                                                                                                                               68.9%; Score 505; DB 1; Length 109; 88.9%; Pred. No. 3.7e-42; ive 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.5%; Score 502; DB 1; Length 10
larity 88.9%; Pred. No. 7.2e-42;
Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11746 MW; 566C115E6B9CBEEE CRC64;
                                                                                                                                                                                                                                                        109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
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HSSP, P80362; 1WTL.

GO, GO:0005576; C:extracellular; NAS.
GO; GO:0006952; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00110; 1g-11ke.
InterPro; IPR00110; 1g-11ke.
Ffam; PF0047; ig; 1.
SWART; SW00406; IGv; 1.
FROSTIT; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DISGUIRD 23 89 BY SIMILBRIT DISGUIRD 23 89 BY SIMILBRIT SEQUENCE 109 AA; 11775 MW; 7689C3ECD6
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SMART; SMO406; 1GV; 1.
PROSITE; PSS5085; 1G LIKE; 1.
Immunoglobulin V region.
DISULFID 23 89 BY
NON TER 109 AA; 11746 MW;
                                                                                                                                                                                                                                                                                                                                            96, Conservative
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Best Local Similarity
Matches 96; Conserv
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Matches 9
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KV3E_HUMAN
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  Pech M., Zachau H.G.;
within the VK locus.";
within the VK locus.";
within the VK locus.";
Wolelec Acids Res. 12:9229-9236(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEAPAQLIFILLIWIPDTTREIVMTQSPPTLSLSPGERVTLSCRASQSVSSSYLTWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               group.";
Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA-GLOBULIN ACTIVITY.
PIR; A01892; K3HUSI.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa,chain V-III region SIE.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primatee; Cararrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PGOAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOK 111
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.0%; Score 506; DB 1; Length 11
88.3%; Pred. No. 3.2e-42;
iive 3; Mismatches 10; Indels
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Best Local Similarity
Matches 89; Conserv
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P04206;
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RX SEQUENCE.

RA State L., Barnikol H.U.; Watanabe S., Hilschmann N.;

RT Tanning of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Timmunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TT I'). The complete antibody production.";

RI The mechanism of antibody production.";

RI Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).

CC -!- MISCELLANBOUS: THE C. REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -!- MISCELLANBOUS: This is a Bence-Jones protein.

DR A0180576; C:extracellular; NAS.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0005576; P:inmune response; NAS.

DR GO; GO:0005576; P:inmune response; NAS.

DR GO; GO:0005576; IG-1ike.

DR SMART; SM00406; IG-1.

DR SMART; SM00406; IG-1.

DR SMART; PS1031; U LIKE; 1.

DR PROSITE; PS50335; IG LIKE; 1.

MITMUNOGIOUDIN V region; Bence-Jones protein.

MITMUNOGIOUDIN V region; Bence-Jones protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Milstein C.;
"The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, Fr4 and B6.";
FEBS Lett. 2:301-304(1969).
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1-JUL-1998 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region B6.
16 kappa chain V-III region B6.
Bukaryota; Metazoa; Chordat; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606,
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DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGRTFGQGTKVEIK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.9%; Score 498; DB 1; Length 109; 88.0%; Pred. No. 1.7e-41; ative 8; Mismatches 5; Indels
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                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-III region Ti.
Homo Sapiens (Human).
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Best Local Similarity
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P01619;
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SEQUENCE
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NEDLINE=86230578; PubMed=3086710;
Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Tread and the second of a light chain variable region of a human
treactivity with antipeptide antibodies.";
Mol. Immunol. 23:139-244(1986).
New P.R., A01893; K3HUGO.
New R.S.P., P80362; LWTL.
New R.S.P., P80362; LWTL.
New R.S.P., P80362; LWTL.
New R.S.P., P80362; P:antigen binding; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:00065576; P:antigen binding; NAS.
New R.S.P., P8036356; P:antigen binding; NAS.
New R.S.P., R.S.P., R.S., R.S
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Score 489; DB 1; Length 10
82.4%; Pred. No. 1.3e-40;
ive 11; Mismatches 8; Indels
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20-MAR-1987 (Rel. 04, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
16 Xappa chain V. Lil region GOL (Rheumatoid factor).
Homo sapiens (Human).
-!- MISCELLANEOUS: This is a Bence-Jones protein. PIR; A01891; K3HUB6. HSSP: P80362; 1HT. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                     InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
PMART; SMO047; ig; 1.
PMOSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Bence-Jones protein.
DISULPID 23 89 BY SIMILARITY.
DISULPID 108 A9; 11635 MW; 8BC14FF07A419E
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KV1W HUMAN
P04431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
"Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
"I small family of germ-line V genes.";

Nature 307:77-80(1984).

-- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.

PIR, A01894; K3HUNG.

RSSP, P80362; 1WTL.

GO, GO:0005576; c:extracellular; NAS.

GO, GO:0005576; c:extracellular; NAS.

GO, GO:0005576; r:extracellular; NAS.

RO, GO:0006555; p:immune response; NAS.

RO, GO:0006955; p:immune response; NAS.
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MEDIINE=76276460; PubMed=60899;
MEDIINE=76276460; PubMed=60899;
MIADPET D.G., Capra J.D.;
"The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IgM anti-gamma globulins.";
Ann. Immunol. (Faris) 127C:261-271(1976).
-! MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
1-JUL-1998 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region NG9 precursor (Fragment).
17 Homo sapiens (Human).
18 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammania; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BY SIMILARITY.
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16-OCT-2001 (Rel. 40, Last annotation update)
19 kappa chain V-III region POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=84093600; PubMed=6419127;
Bentley D.L.;
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21-JUL-1986 (Rel. 01, Last seq
16-OCT-2001 (Rel. 40, Last ann
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KV3F HUMAN
P01624;
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                                                                                                               HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 BIALTOSPGTLSLSPGERATLSCRASOSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=85014148; PubMed=6091049;

Klobeck H.G., Combriato G., Zachau H.G.;

Klobeck H.G., Combriato G., Zachau H.G.;

"Immunoglobulin genes of the Kappa light chain type from two human

"Immunoglobulin genes of closely related.";

Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Last sequence update)
15-AUG-1987 (Rel. 06, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region Walker precursor.
16 bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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PRANTWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMDWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOKYGTSAITFGOGTRLEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ARFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPPTFGQGTRVEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 447; DB 1;
Pred. No. 1.5e-36;
8; Mismatches 13;
                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
HSSP, P80362; IWTL.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
Ffam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
FROSITE; PS50815; IG LIKE; 1.
Immunoglobulin V region.
DISGUIPID 23 89 BY SIMILARIT NON TER 109 109
SEQÜENCE 109 AA; 11922 MW; 62821DDC6A.
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PIR; A01883; X1HUWK.
HSSP; POLGO7; LEX.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
PFam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                       61.0%;
80.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                  1;
                                                                                                                                                                                                                                   61 PGQAPRILIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
                                                                                                                                                                                                                                                       1 METPAQLLFLLLLMLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK 60
                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 07, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-IV region B17 precursor.
Homo sapiens (Human).
Eikaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marsh P., Mills F., Gould H.;
"Detection of a unique human V kappa IV germline gene by a cloned cDNA probe.";
                                                                                                                58.3%; Score 427.5; DB 1; Length 129; 66.4%; Pred. No. 1.4e-34; ive 16; Mismatches 26; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG KAPPA CHAIN V-IV REGION B17.
PRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMENORK-2.
               FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
 COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marsh P.; Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                             119 COMPLEMENTARITY-DETERMININ
129 FRAMEWORK-4.
110 BY SIMILARITY.
129 MW; F941FA07D4AFC2F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:000695; P:immune response; NAS. InterPro; IPR007110; IG-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 13:6531-6544(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=86041854; PubMed=2997713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; iGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X02990; CAA26733.1; -. HSSP; P80362; 1WTL.
                                                                                                                Query Match
Best Local Similarity 66.4%
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                            QGTRLEIK 128
                                                                                                                                                                                                                                                                                                                          QGTRLEIK 129
                               111
120
45
129
129 AA;
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P06314;
                                          DOMAIN
DISULFID
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SEQUENCE
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KV4C HUMAN
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61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL 120
                                                                                                                                                                                                                    56 WYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS 115
                                                                                                                                                                 55
                                                                                                                                                                               1 MVLQTQVFISLLLMISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLA 60
                                                                                                                                                               1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSF----SSSYLA
                                                                                                                                     5; Gaps
                                                                                                       Query Match 57.4%; Score 420.5; DB 1; Length 134; Best Local Similarity 60.9%; Pred. No. 7.1e-34; Matches 81; Conservative 20; Mismatches 27; Indels 5;
              FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
COMPLEMENTARITY-DETERMINING-2
                                                                               14966 MW; 6413A22FD0738832 CRC64;
                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                        116 AITFGQGTRLEIK 128
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82
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1224
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Search completed: April 5, 2004, 13:24:55 Job time : 6.48731 secs

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Catarrhini, Hominidae, Homo.
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1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fetus.",
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, A705036, AAD56272.1; -.
PIR, A30601, A30601.
PIR, A30601, B30601.
PIR, B30601, B30601.
PIR, B30601, B30601.
PIR, B30601, B30601.
PIR, C30601, C30601.
PIR, C30601, C30601.
PIR, C30601, C30601.
PIR, C30601, C30601.
PIR, B30601, B30601.
PIR, B30601, B30601.
PIR, B30601, B30601.
PIR, B30601, B30601.
PIR, B30601, F30608.
PIR, B30601, F30608.
PIR, B30601, F30608.
PIR, B30601, B30608.
PIR, B30601, B30601.
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              Q9UL70
Q91WP8
Q91WP8
Q9UL77
Q9UL77
Q9UL77
Q9UL81
Q9UL81
Q9UL81
Q9UR9
Q91WS9
Q91
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QSKOFS
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
NCBI_TaxID=9606;
                                                                                                                                                                                                                          4444444444
RESULT 1
09UL78
ID 09UL78
AC 09UL78;
Q9ul78 homo sapien
Q7a473 homo sapien
Q7a2y4 homo sapien
Q7a2y4 homo sapien
Q8tcd0 homo sapien
Q8tcd0 homo sapien
Q7a36 xenopus lae
Q9ul83 homo sapien
Q7tmk3 mus musculu
Q7ts98 mus musculu
Q7ts98 mus musculu
Q8vci6 mus musculu
                                                                                                 April 5, 2004, 13:24:21; Search time 30.2741 Seconds (without alignments) 1479.931 Million cell updates/sec
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733
1 METPAQLLFLLLLMLPDTTG......TRLEIKGTVAAPSVFIFPPS 142
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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072473
09U286
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09U880
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07TWX3
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079M37
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079M37
079W39
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seg length: 200000000
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Match 1
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Perfect score:
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Maximum DB
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No.
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Query Match

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072473; Q7Z473

Q72473

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60 PGKAPQLLIYAASTLQSGVPSRFSGSASGTDFTLSISCLQSEDFATYYCQQXYTYPWTFG 119
                                                                                                                                                                                   61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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                                                             1 METPAQLLFLLLLWLPDTTGETALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                              Craniata, Vertebrata, Euteleostomi;
Catarrhini; Hominidae; Homo.
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1-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
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29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Immunol. Immunopathol. 87:184-192 (1998)
EMBI, APO35028, AAD55028, AAD56264.1; -.
PIR, B30607; B30607.
PIR, I30601; I30601.
14; Mismatches
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                                                                                                                                                                                                                                                                                                                 121 OGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                         120 QGTKVEIKRTVAAPSVFIFPPS 141
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P80362, IWTL.
InterPro, IPR007110, Ig-like.
InterPro, IPR003596, Ig.v.
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   98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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   Matches
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Q7Z3Y4
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MEDLINE=2238257; PubMed=12477932;

MILLINE=2238257; PubMed=12477932;

MILLINE=2238257; PubMed=12477932;

MILLINE=2238257; PubMed=12477932;

MILLINE ALL Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

ALtschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A Brownsein M.J., Uodun T.B., Toshiyuki S., Carninoi P., Prange C.,

RA And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Rohards S., Worley N., Scherrs G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley N., Sodergren B.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Murny D.M., Schergren B.J., Lu X., Gibbs R.A.,

R William A., Youchman A., Young A.C., Shevohenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Richards M. M., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

R Richards M. M., Shalska U., Smallus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 EIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO56256; AAH56256.1; -.
Hypothetical protein.
SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BCOF CRC64;
                                                                                                                                                                                                                                                                                                                                                  SF675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                            Score 505; DB 4; L
Pred. No. 1.1e-44;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                    HSSP, P80362, 1WTL.
INCERP:0; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Pfan; PF00047; Ig, 1.
SMART; SW00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                 109 109
109 AA; 11646 MW;
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89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97; Conservative
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                                     PH0965; PH0965.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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01-OCT-2003 (
01-OCT-2003 (
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Gaps

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61 YLQKPGQSPQLLIYLGSNRASGVPDRPSGSGSGTDFTLKISKVBAEDVGIYYCMQGLQTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 YQQXPQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSA 116
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 239
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58.9%; Pred. No. 1.6e-38;
iive 27; Mismatches 29; Indels
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 2.
SMART; SM00407; IGC1, 1.
SMART; SM00407; IGC1, 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
HYDOLHerical protein.
SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 ITFGQGTRLEIKGTVAAFSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 OTFGQGTKVEIKRTVAAPSVFIFPPS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
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Mammalia; Butheria; Primates;
NCBI_TaxID=9606;
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Best Local Similarity 58.98
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                     Query Match
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Q8TCD0
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                                                                           MEDLINE=228825; PubMed=12477932;

MEDLINE=228825; PubMed=12477932;

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MELLINE=228825; PubMed=12477932;

MELLINE=228825; PubMed=12477932;

MELLINE=228825; PubMed=12477932;

MELLINE R.P., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

MELLINE R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

MELCHORKO L., Marusina K., Farmer A., Rubin G.M., Hong L.,

MELCHORKO L., Marusina K., Farmer A., Rubin G.M., Hong L.,

MELCHORKO L., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MICHAGA S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MICHAGA S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milchop D.K., Wuzuy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milchop M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milchop M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milchop M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milchop M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milchop M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milchop M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Marzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.,

Maria M.A., Madan A., Young A.C., Smailus D.E., Schnerch A., Schein J.E.,

Mannes S.J., Marra M.A.,

Mannes S.J., Marra M.A.,

Mannes S.J., Marra M.A.,

Mannes S.J., Marra M.A.;

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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.6%; Score 473.5; DB 4; Length 236; 65.5%; Pred. No. 5.8e-41; ive 19; Mismatches 29; Indels 1
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC030814; AAH30814.1; -.
PIR; S23638; S23638.
PIR; S34091; S34091;
PIR; S40357; S40357.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; 2001) to the EMBL/GenBank/DDBJ databases. Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EC005332; AAH05332.1; -. Hypothetical protein. SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBNEKO
QBNEKO;
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OBNEKO

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121 STFGQGTKLEIKRTVAAPSVFIFPPS 146

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(Fragment)
                                                                                                                                                                                                                                                                                                            Fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                  Q9UL83
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09UL85
RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Bonaldo M.F., Carainor B.L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carainor B.L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodriques S., Sanchez A.,

RA Halton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Boutfeard G.G.,

RA Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Nodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human manner and selective and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 VPKLLIYLANTRHTGTPERISGSGSGTDFTLTISRMEAEDAADYYCQQSRSDPLTFGKGT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 APRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LLFLLLLWLPDTTGEIALTQSPGTLSLSPGBRATLSCRASQSF---SSSYLAWYQQKPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Gaps
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match ' 58.0%; Score 425.5; DB 13; Length Local Similarity 61.2%; Pred. No. 5.6e-36; es 85; Conservative 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC054155; AAH54155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26300 MW; 47B8D0D2639CB436 CRC64;
                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                   01-0CT-2003 (TYEMBLRE). 25, Created)
01-0CT-2003 (TYEMBLRE). 25, Last seg
01-0CT-2003 (TYEMBLRE). 25, Last ann
Hypothetical protein.
Xenopus laevis (African clawed frog)
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 RLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dev. Dyn. 225:384-391(2002)
                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 237 AA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
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Best Local Si
Matches 85;
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                                                                                                                Q7SZ36
                                     RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQQKPGQAPRLLIYCASTRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                           Indunyo sayrema (mangara).
Eukarota, Metazona:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Myosin_reactive autoantibodies in rheumatic carditis and normal
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ARFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOKYGTSAITFGOGTRLEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.,
                                                                                                                                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 57.9%; Score 424.5; DB 4; Local Similarity 78.7%; Pred. No. 2.5e-36; es 85; Conservative 8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL, AF035031; AAD56267.1; -.
PIR, B30609; B30609.
PIR, C30609; D30609.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR, 534098; 834098.
PIR, 334099; 834099.
HSSP, P80362, 1MTL.
INTERPO; IPR007110; IG-like.
InterPo; IPR03596; Ig_v.
Ffam; PR00404; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQXYGTSAITFG 120
                                                                                                              62 PWKSPKTLIYYATSLADGVPSRFSGSGSGQDYSLTISSLESDDTATXYCLQHGESPYTFG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 YQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METPAQLIFLILLWIPDTTGEIALTQSPGTLSLSPGERATLSCRASQSF----SSSYLAW 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 MRAPAQFEGILLLWFPGIRCDIMUTQSPSSMYASLGBRVTITCKASQDI-KSYLSWYQQK 61
              1 METPAQLLFLLLUMLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                              238 AA.
                                                                                                                                                                           121 QGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                             ||:|||| |||||
122 SGTKLEIKRADAAPTVSIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1191; 25-DEC-02.
PDB; 1LO2; 31-JUL-02.
PDB; 1LO4; 31-JUL-02.
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$24536; $24536.
$24538; $24538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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S24533;
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Matches
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PIR;
PIR;
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                                                                                                                                                                                                                                                                           RESULT 11
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STRAINCECECH II, TISSUE-Breast tumor;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; MAX 51.1, MAX 51.1, MAM 51.1, MAM
                                                                                                                                                                                                                                                                             ;
7
                                                                                                                                                                                                                                                                                                                                                1 EIVWTQSPATLSVSPGERATLSCWASQSISSN-LAWYQQKPGQAPRLLIYGASTRATGIP 59
                                                                                                                                                                                                                                                                                                                21 BIALTOSPGTLSLSPGERATLSCRASOSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIP 80
                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                    ARFSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                             81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGT-SAITFGQGTRLEIK 128
                                                                                                                                                                                                                               Query Match 57.6%; Score 422; DB 4; Length 109; Best Local Similarity 77.1%; Pred. No. 4.7e-36; Matches 84; Conservative 12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R., Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055906; AAH55906.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypochetical protein.
SEQUENCE 236 AA; 26299 MW; 0DB03488AAA6396F CRC64;
                                                                                                                                                                                           109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Buse musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CZECH II; TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                               HSB), P80362, 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Fram; PF00047; ig; 1.
SWART; SW00406; IGv; 1.
PROSITE; PS50815; IG LIKE; 1.
EMBL; AF035029; AAD56265.1;
PIR; D30609; D30609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                           109
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Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse
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SEQUENCE
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07TMK3
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Gaps

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PRT;
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                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54...
Best Total Similarity
Total Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                        PIR, S07455, S07455.
PIR, S16112, S16112.
PIR, S26334, S26334.
PIR, S60066, S60066.
                                           D29380.
E28833.
F32530.
H31485.
                                                                                       PH0106.
PH1030.
PH1031.
                                                                                                                                      PL0257.
PT0359.
                                                                                                                         PH1034
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                                           D29380; I
E28833; I
F32530; I
                                                                                                                                      PL0257;
PT0359;
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                                                                             H31485;
PH0106;
                                                                                                    PH1030;
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SEQUENCE 2:
                                                                                                                         PH1034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPRTFG 121
60 YLQKPGQSPKILIYKVSNRFSGVPDRPSGSGSGTDFTLKISRVEAEDLGVYYCFQCSHVP 119
                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                    01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-colorectal carcinoma light chain.
Buks musculus (Mouse).
Euksrycta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDINNE-9383497, FubMed=8372513;
Tonge D. Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
"Cloning and characterization of 1116NS19.9 heavy and light chain cDNAs and expression of antibody fragments in Bscherichia coli.";
Sear Immunol. 7.566-22(1993).
EMBL; S65921; AAB28160.1; -.
SEQUENCE 236 AA; 26454 MW; 2C586EBFSEA10F4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                           56.3%; Score 412.5; DB 11; Length 236; 56.3%; Pred. No. 1.3e-34; ive 22; Mismatches 39; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 AA
                                                                                                                236 AA
                                    117 ITFGQGTRLEIKGTVAAPSVFIFPPS 142
                                                 120 YTFGSGTKLEIKRADAAPTVSIFPPS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GGTKLEIKRADAAPTVSIFPPS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8VCI6 PRELIMINARY;
Q8VCI6 01-MAR-2002 (TrEMBLrel. 20, C3
01-MAR-2002 (TrEMBLrel. 20, L6
01-OCT-2003 (TrEMBLrel. 25, L6
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Colon;
Strausberg R.;
Submitted (DEC-2001) to the E
EMBL; BC019760; AAH19760.1; -
PIR; A27887; A27887.
                                                                                                                                                                                                                                                                                                                                                                   80; Conservative
                                                                                                                PRELIMINARY;
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B27887; B27887.
B30577; B30577.
B31485; B312485.
B32248; B32248
                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                               Q7TS98
Q7TS98;
                                                                                           RESULT 12
                                                                                                     Q7TS98
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57 YOOKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOKYGTSA 116
                                                                                                                                                                                                                                                                                                                                                      60 YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVP 119
                                                                                                                                                                                                                                     1 METPAQLLFLLLIWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSF----SSSYLAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                              55.5%; Score 406.5; DB 11; Length 238; 54.1%; Pred. No. 5.3e-34; ive 29; Mismatches 33; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ED019474; AAH19474.1; -.
PIR; B47329; B47329.
InterPro; IPR007010; Ig-like.
InterPro; IPR00306; Ig-V.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG-LIKE; 2.
PROSITE; PS50835; IG-LIKE; 2.
Hypothetical protein.
l protein.
238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          117 ITFGOGTRLEIKGTVAAPSVFIFPPS 142
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Mon Apr 5 14:16:19 2004
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18-10-044-5645-4:rsD

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57 YOOKPGQAPRILIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCOKYGTSA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
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OBVC55;

O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 25, Last annotation update)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein.

Mus musculus (Mouse).

Bukaryocta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

CTT TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                Query Match 55.3%; Score 405.5; DB 11; Length 234; Best Local Similarity 57.7%; Pred. No. 6.6e-34; Matches 82; Conservative 18; Mismatches 41; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.2%; Score 390; DB 11; Length 239; Best Local Similarity 53.4%; Pred. No. 2.7e-32; Matches 78; Conservative 27; Mismatches 37; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Straubberg R.;
Submitted (GAN-2002) to the EMBL/GenBank/DDBJ databases.

Lubmitted (GAN-2002) to the EMBL/GenBank/DDBJ databases.

R PIR, A3393; A3393.

R PIR, A3993; A3393.

R PDB; IKC5; 24-UUL-02.

GO; GO:0015070; F:toxin activity; IEA.

R GO; GO:0015070; F:toxin activity; IEA.

R GO; GO:001405; P:pathogenesis; IEA.

InterPro; IPR00410; Ig-like.

R InterPro; IPR003106; Ig_MHC.

R InterPro; IPR003106; Ig_WHC.

R InterPro; IPR00306; Ig_W.

R Pfam; PF00250; Conotoxin; 1.

R Pfam; PF00047; ig; 2.

R Pfam; PF00040; ig; 2.

R PROSITE; PS50835; IG_LIKE; 2.

R PROSITE; PS50835; IG_LIKE; 2.

R PROSITE; PS00030; IG_MHC; 1.

R PROSITE; PS00030; IG_MHC; 1.
234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
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                                                                                                                                                                                                                                                         120 SGTKLEIKRADAAPTVSIFPPS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Colon;
 SEQUENCE
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Q8VC55
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April 5, 2004, 12:09:21 ; Search time 45.8917 Seconds (without alignments) 874.270 Million cell updates/sec
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733
1 METPAQLLFLLLLWLPDTTG......TRLEIKGTVAAPSVFIFPPS 142
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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A_Geneseq_29Jan04:*
1: _geneseqp1980s:*
2: _geneseqp200s:*
4: _geneseqp2001s:*
5: _geneseqp2001s:*
6: _geneseqp2003s:*
7: _geneseqp2003bs:*
8: _geneseqp2003bs:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab47060 Light cha	377	Aay93702 The kappa	3729 The	384 Huma	1366 Anti-C	181	Aau74299 Anti-huma	Aab47061 Light cha	79	04 The	31 The	86 Huma	01 Anti-1	Aay93733 The kappa	08 The	88 Huma	Aaw40069 Human mon	Aae00946 Human mon	ις L	Abj36930 Anti-CD40	Aay92239 Human bon	Ade28473 Human ant	Aar38672 vk325-Jk2	1155
1D	AAB47060	AA018877	AAY93702	AAY93729	AAE35884	ABP71366	ADE28481	AAU74299	AAB47061	AA018879	AAY93704	AAY93731	AAE35886	AAU74301	AAY93733	AAY93708	AAE35888	AAW40069	AAE00946	ABU10485	ABJ36930	AAY92239	ADE28473	AAR38672	AAW11155
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Length	4	4	m	235	m	m	m	m	4	4	m	m	m	m	ന	S	m	ហ	ഗ	S	m	m	ო	a	m
% Query Match	100.0	100.0		93.0												88.7					86.8				
Score	733	m	ဏ	682	8	999	58	658.5	2,4	Ŋ	654	654	654	ന	50	650.5	50	649	649	641	636	93	~	625	624.5
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Abp57366 Anti-TRAI Abr41582 Human DIT Ada43061 Human ant		C		Aao14066 Light cha Abu08018 Human mon Aau33249 Novel hum Aar38650 Human V-k
ABP57366 ABR41582 ADA43061	AAR41286 ADD01357 AAG71272	ABG03490 ADC61062 AAM24101 AAK52951 AAW345439	AAU14462 AAU14463 AAU14461 AAU14461	AAO14066 ABU08018 AAU33249 AAR38650
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133		4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	234 234 178 116
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620.5 615 614	600 600	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 W W W W	589.5 589.5 583.5 574
9 7 8 9	, w w w v	ა	. w w 4. 4.	4 4 4 4 ሪ 6 4 ቢ

ALIGNMENTS

AC AAB47060;	
DT 08-MAY-2001	(first entry)
Light	chain variable region VL of BO2C11.
AA KW Monoclonal an	antibody; variable region; heavy chain; light chain; VH; VL;
	complementarity determining region; CDR; MAb; BO2C11;
KW arterial rest	arterial restenosis; venous thrombosis; arteriosclerosis.
OS Homo sapiens.	
AA FH Kev	Location/Oualifiers
	43.54
FT Domain	/label= cDri 6975
FT FT Domain	/label= CDR2 109117
FT	/label=:CDR3
PN WO200104269-A1	1.
PD 18-JAN-2001.	
AA PF 13-JUL-2000;	2000WO-EP006677.
XX PR 14-JUL-1999; PR 14-JUL-1999;	99GB-00016450. .99US-0143891P.
XX PA (LEUV-) LEUVEN	IN RES & DEV VZW.
XX PI Jacquemin MG,	Saint-Remy JR;
XX DR WPI; 2001-138333/14 DR N-PSDB; AAC85453.	333/14. 453.
	Novel cell lines for producing monoclonal antibodies that bind to a factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.
XX PS Example 5; Fi	Fig 7; 55pp; English.

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N-PSDB; AAA46865.
                                                   N-PSDB; AAL49255
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 142 AA;
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This sequence represents the light chain variable region of the human monoclonal antibody (MAb), BO2C11. BO2C11 is a human MAb which recognises a conformational epitope within the carboxy-terminal of the factor VIII light chain. BO2C11 recognises both the wild type and Arg2150fis factor VIII light chains. The MAb produced by the cell line of the invention, KRIXI, specifically recognises the wild type factor VIII light chain. Second to inhibit the binding of factor VIII light chain. KRIXI is deposited factor in a dose dependant manner. The new cell line KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder or thrombolic pathologic condition such as intravascular coagulation, arterial thrombosis, arterial restenosis, venous thrombosis or arteriosclerosis, and attenuation of coagulation in ammmal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly in humans
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100.0%; Score 733; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 142; Conservative 0; Mismatches 0;
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/label= CDR1
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The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic Inflammatory response syndrome (SIRS), espsis, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an active ingredient a partial inhibitor of factor VIII, in admixture with a cartive intravascular nonlude the antibodies B02011 and KRIXI. The present sequence is the light chain variable region of B02011
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containing specified heavy and light chain sequences, useful for
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Pharmaceutical composition for treating systemic inflammatory response syndrome, sepsis, septic shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor VIII.
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100.0%; Pred. No. 2.9e-42;
ive 0; Mismatches 0;
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                                                                                                                                                                                        Disclosure; Fig 11; 41pp; English
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Best Local Similarity 100.
Matches 142; Conservative
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Homo sapiens
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                                     The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antipled.

4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to used to uperliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to uperliferative disorders (e.g. cancer).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
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Pred. No. 1.2e-38;
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6; Mismatches
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e.g. immune disorders.
                   Claim 3; Fig 1A; 157pp; English.
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Matches 131, Conservative
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N-PSDB; AAA46893.
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                                                                                                                                                               Sequence 235 AA;
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treating,
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Peptide
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invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)

4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a RRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient
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                                                                                                                                     The present sequence represents a kappa chain of an antibody of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
-4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
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Pred. No. 1.2e-38;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 4.1.1 anti-CTLA-4 antibody kappa chain.
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/label=_Signal_peptide
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                                                                                                        Claim 3; Fig 22g; 157pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.0%;
llarity 92.3%;
Conservative
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Best Local Similarity
Matches 131; Conserv
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90.9%;
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Best Local Similarity 90.1
Matches 128; Conservative
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                                                                                                                                                                                    Sequence 235 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibodies that interact with osteoprotegerin ligands, useful for treating osteopenic disorders, e.g. osteoporosis, bone loss from arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and
                                     The invention relates to the use of human anti-cytotoxic I lymphocyte antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for the treatment of cancer such as bone cancer, pancreatic cancer, skin cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian cancer, cancer of the anal region, stomach cancer, breast cancer, cesticular cancer and carcinoma of the fallopian tubes. The present sequence is human anti-CTLA-4 antibody kappa chaln
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                                                                                                                                                                                    METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                        Osteoprotegerin ligand, osteopathic, antiinflammatory, antirheumatic, antiarthritic, cytostatic, OPGL, anti-OPGL-1, antibody.
                                                                                                                                                                Gaps
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preparation of medicament for the treatment of cancer.
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Pred. No. 1.2e-38;
6; Mismatches 5;
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/note= "variable region"
129. .235
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                   76pp; English.
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                                                                                                                                           93.0%;
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                                                                                                                                          Query Match
Best Local Similarity 92.3
Matches 131; Conservative
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/note=
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                   Disclosure; Fig 1G;
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                                                                                                                       Sequence 235 AA;
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Peptide
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anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; fimunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; light chain; 24-2-1.
                                                    The invention relates to antibodies that interact with osteoprotegerin ligands (OPGL). The antibody is useful for detecting the level of OPGL in a biological sample. The antibody, or the pharmaceutical composition comprising the antibody, or the pharmaceutical composition an inflammatory condition with attendant bone loss, an autoimmune condition with attendant bone loss in a patient or rheumatoid arthritis in a patient. In particular, the antibody or composition is useful for treating bone diseases, e.g. osteoporosis, bone loss from arthritis. Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's syndrome or acromegaly), osteogenesis imperfecta, homocystinuxia, Menkes' syndrome, Xiley-Day syndrome, osteomyelitis, hypercalcemia, or nibody kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QGTRLEIKGTVAAPSVFIFPPS 142
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Claim 1; Fig 4; 144pp; English
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV such as cancer, virucide, and bacterial, immunostimulant and anti-HIV such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length light chain protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQY-SSLFTFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 METPAQLIFILILMILPDITGEIVLTQSPGTLSLSPGERATLSCRASQSVSSTYLAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; hepatororopic; activation inducible lymphocyte immunomodulatory molecule; AllIM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; graft versus host reaction; immune rejection; intestinal immunity; ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-human AILIM monoclonal antibody clone Jmab-138, light chain.
                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 234;
                                                                                                                                                                                                                                                                                                                                                                89.8%; Score 658.5; DB 7;
90.1%; Pred. No. 4.7e-37;
ive 7; Mismatches 6;
                                    Claim 7; SEQ ID NO 88; 177pp; English.
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30-MAR-2001; 2001JP-00099508.
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Matches 128; Conservative
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N-PSDB; AAS99475.
viral infections.
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The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomedulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, and for inducing antibody-dependent cytocoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells. (I) is useful for treating and preventing various diseases associated with AILIM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the cheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, systematosis, autoimmune or allergic diseases, inflammatory dermatosis, psoriasis, autoimmune or allergic disease, inflammatory dermatosis, intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreative colitis, pneumonia, hepatitis, and pancreaticis. (I) induces no serious anti-human anti-monoclonal antibody amino acid sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 METPAQLLFLLLLWLPDTTGETALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
               New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.8%; Score 658.5; DB 5; Length 236;
89.5%; Pred. No. 4.7e-37;
live 8; Mismatches 6; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain variable region VL of KRIX1.
                                                                                                                   Claim 30; Page 284-285; 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GQGTRLEIKGTVAAPSVFIFPPS 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB47061 standard, protein, 143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43. .54
/label= CDR1
69. .75
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 89.5
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB47061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Domain
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The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic inflammatory response syndrome (SIRS), sepsies, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an active ingredient a partial inhibitor of factor VIII, in admixture with a cartive input of short inhibitors may include the antibodies B02011 and KRIXI. The present sequence is the light chain variable region of KRIXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSA-ITF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 METPAQLIFILILIMEPDITGEIVITQFPGTLSLSPGERATISCRASQSVASAXLAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pharmaceutical composition for treating systemic inflammatory respons syndrome, sepsis, septic shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor VIII.
complementarity determining region; antibacterial; antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 654.5; DB 5;
Pred. No. 5.7e-37;
7; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The kappa chain of immunoglobulin clone 4.8.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 13, 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93704 standard; protein; 233
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                                                                                                                                     69. .75
/label= CDR2
108. .117
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.3%;
                                                                                                                                                                                                                                                                                                                    11-JAN-2002; 2002EP-00447005.
                                                                                                                                                                                                                                                                                                                                                                                                  (COLL-) COLLEN RES FOUND VZW
                                                                                                                    CDR1
                                                                                                                                                                                                                                                                                                                                                            11-JAN-2001; 2001US-0261405P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                     43. .54
/label= (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-610270/66.
N-PSDB; AAL49257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacquemin MG,
                                                                                                                                                                                                                                        EP1222929-A2
                                          Homo sapiens
                                                                                                                                                                                                                                                                                17-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                Key
Region
                                                                                                                                                                                 Region
                                                                                                                                           Region
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      Z Z X B X B X B X B X B B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the light chain variable region of the monoclonal antibody (MAb), KRIXI. This MAb produced by the cell line of the invention, specifically recognises the wild type factor VIII light chain. KRIXI can be used to inhibit the binding of factor VIII light distriction in a dose dependant manner. The new cell line KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder or thrombocits pathologic condition such as intravascular coagulation, arterial thrombosis, venous thrombosis or arteriosclerosis, and attentation of coagulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSA-ITF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, antibody, B02C11, KRIX1, light chain, heavy chain, inflammation, variable region, factor VIII inhibitor; sepsis, septic shock, thrombus formation, systemic inflammatory response syndrome; CDR, disseminated intravascular coagulation, haemophilia A, immunosuppressive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLIFILLIMLPDITGEIVLIQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 METPAQLIFILLIMIPDITGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                             Novel cell lines for producing monoclonal antibodies that bind to factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 654.5; DB 4;
Pred. No. 5.7e-37;
7; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human KRIX1 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GGGTKVEIKRTVAAPSVFIFPPS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Fig 9; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA018879 standard; protein; 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.3%;
89.5%;
                                                                                                                                                                               99GB-00016450.
                                                                                                                                                                                                                                                                                Saint-Remy JR;
                                                                                                                                         13-JUL-2000; 2000WO-EP006677
                                                                                                                                                                                                                                      (LEUV-) LEUVEN RES & DEV VZW
    109. .118
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.5
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                    WPI; 2001-138333/14.
N-PSDB; AAC85454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 143 AA;
                                                             WO200104269-A1
                                                                                                                                                                                                                                                                                Jacquemin MG,
                                                                                                                                                                               14-JUL-1999;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2002
                                                                                                   18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA018879;
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      Domain
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Davis CG;

Gilman SC,

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The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytofoxic T-Imphocyte antipaen (CTLA) 4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft redjection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be eged to up-regulate immune system to up-regulate immune system to up-regulate immunodeficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISPFTFG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGQAPRLLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METPAQLLFLLLMLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRT--SVSSSYLAWYQOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 654; DB 3; Length 23
Pred. No. 9.4e-37;
1; Mismatches . 8; Indels
                                                                                                                                                                                                                                                                                                                  Hanke JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-CTLA-4 antibody kappa chain.
              Location/Qualifiers
1. .20
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GGTKVEIKRTVAAPSVFIFPPS 140
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                                                                                                                                                                                                                                                                                                                  Mueller EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 22k; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.2%;
90.1%;
                                                                                                                                                                            99WO-US030895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                    Neveu MJ,
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-442647/38.
                                                                                                                                                                                                                                                      (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA46895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 233 AA;
                                                                                               WO200037504-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-2003
                                                                                                                                                                            23-DEC-1999;
                                                                                                                                                                                                                  23-DEC-1998;
                                                                                                                                                                                                                                                                                                                    Hanson DC, Corvalan JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 4.8.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128;
                                                                                                                                     29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                     Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antibody -4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VRB-33 family gene. The modifications are contained in cDR2, and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                        (CTLA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METPAQLLFLLLMLPDTTGEIVLTQSPGTLSLSPGERATLSCRT--SVSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                 Davis CG;
                                                                                                                                                                                                                                                                                                                                                                                                               Novel antibodies capable of binding cytotoxic T-lymphocyte antigen -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 654; DB 3; Length 233; Pred. No. 9.4e-37; Aismatches 8; Indels
                                                                                                                                                                                                                                                                                               Gilman SC,
proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                               Hanke JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The kappa chain of immunoglobulin clone 4.8.1.
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                                                                                                                                                                                                                                                                                                 Mueller EE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY93731 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 1B; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.2%;
90.1%;
                                                                                                                                                           99WO-US030895.
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                                                                                                                                                                                                                                                                                                 Neveu MJ,
                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-442647/38.
N-PSDB; AAA46867.
                                                                                                                                                                                                                                                        ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                     (PFIZ ) PFIZER INC (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 233 AA;
                                                                              WO200037504-A2
                                          Homo sapiens
                                                                                                                                                                                                 23-DEC-1998;
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                                                                                                                                                           23-DEC-1999;
                                                                                                                                                                                                                                                                                               Hanson DC, Corvalan JR;
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AAY93731;

AAY9373

Homo

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Query Match

Best Loca Matches

9 28

Gaps

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Length 233;

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ulcerative colitís; pneumonia; nephritis; vasculitis; pancreatitís.
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                                                                                                                               18-MAY-2000; 2000JP-00147116
30-MAR-2001; 2001JP-00099508
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                                                                                                                                                                         (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 89.5
Matches 128; Conservative
                                                                                                                                                                                                 Tsuji T, Tezuka K,
                                                                                                                                                                                                                           WPI; 2002-075313/10.
N-PSDB; AAS99477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 236 AA;
                                                    WO200187981-A2
                            Homo sapiens.
                                                                               22-NOV-2001
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AAY93733
ID AAY93'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                           The invention relates to the use of human anti-cytotoxic T lymphocyte antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for the treatment of cancer such as bone cancer, pancreatic cancer, skin cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian cancer, cancer of the anal region, stomach cancer, breast cancer, testicular cancer, uterine cancer and carcinoma of the fallopian tubes. The present sequence is human anti-CTLA-4 antibody kappa chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiallergic; antiuleer; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; hepatotropic; activation inducible lymphocyte immunomodulatory molecule; AILIM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic context-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; graft versus host reaction; immune rejection; intestinal immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 METPAQLLFLLLLMLPDTTGEIVLTQSPGTLSLSPGERATLSCRT--SVSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                             Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the preparation of medicament for the treatment of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-human AILIM monoclonal antibody clone Jmab-139, light chain.
                                                                    /note= "Mature anti-CTLA-4 antibody kappa chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 89.2%; Score 654; DB 6; Length 233; Best Local Similarity 90.1%; Pred. No. 9.4e-37; Matches 128; Conservative 4; Mismatches 8; Indels
                            1. .20
/label= Signal peptide
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               Location/Qualifiers
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                                                                                                                                                                          23-MAY-2001; 2001US-0293042P
                                                                                                                                                  23-MAY-2002; 2002EP-00253652
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                                                                                                                                                                                                    (PFIZ ) PFIZER PROD INC.
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N-PSDB; AAD54346.
                                                                                                                                                                                                                               Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 233 AA;
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                                                                                             EP1262193-A1
                                                                                                                       04-DEC-2002
                                                                                                                                                                                                                                Hanson DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU74301;
                            Peptide
                                                       Protein
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The invention relates to a novel human antibody (I), preferably a human monctlonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells (I) is useful for treating, preventing or prophylaxis of delayed type allergy. (I) is useful for treating and preventing various diseases associated with AILIM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the massocial arthitis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, systemic lugus erychematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic disorders inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, vasculitis, and pancreatives. (I) induces no serious commune or allergic disorders colitis, pneumonia, hepatitis, intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, chemically in monoclonal antibody amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGQAPRULIYGASTRATGIPDRRSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAI-TF 119
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New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
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89.5%; Pred. No. 1e-36;
iive 8; Mismatches
                                                                                                                                                                                                         Claim 30; Page 298-299; 300pp; English.
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AAY93733;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
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                                                                                                 Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
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                                                                 The kappa chain of immunoglobulin clone 6.1.1.
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/note= "signal peptide"
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                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 220; 157pp; English.
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                                 03-OCT-2000 (first entry)
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N-PSDB; AAA46897.
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                                                                                                                                                                                                                                                                                 WO200037504-A2
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Corvalan JR;
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                                                                                                                                                                             Homo sapiens
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US-10-291-265-807
US-09-848-832-4
US-10-307-425-1088-4
US-10-307-762-91
US-10-307-762-93
US-10-307-762-93
US-10-201-265-332
US-10-291-265-334
US-09-453-234-86
US-09-453-234-86
US-09-453-234-98
US-09-453-234-98
US-09-453-234-74

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1 METPAQLIFULLIMLPDTTG......TRLBIKGTVAAPSVFIEPPS
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| cgn2_6/prodate/2/pubpaa/PCT_PUBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/PCT_PW_PUB.pep:*
| cgn2_6/prodate/2/pubpaa/PCT_PW_PUB.pep:*
| cgn2_6/prodate/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/prodate/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/prodate/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/prodate/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/prodate/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/prodate/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/prodate/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2 US-10-153-382-7

2 US-10-153-382-7

US-09-859-053-34

4 US-10-044-569B-8

4 US-10-044-569B-8

4 US-10-153-382-11

US-09-782-397-5

1 US-09-782-397-5

1 US-09-782-397-5

1 US-10-203-762-95

5 US-10-309-762-95

5 US-10-291-265-806

5 US-10-291-265-806
                                                                                                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                   1071436 segs, 262597696 residues
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                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                protein search, using sw model
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length: 2000000000
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Match 1
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Maximum DB seq
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                                                                protein
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (325)...(351)
CTHER INFORMATION: complementary determining region number three
US-10-044-569B-4
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (2057..(225)
OTHER INFORMATION: complementary determining region number two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 142;
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (127)..(162)
OTHER INFORMATION: complementary determining region number
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100.0%; Pred. No. 2.9e-55;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 142; Conservative
                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Appli
Sequence 7, Appli
Sequence 34, Appli
Sequence 8, Appli
Sequence 11, Appli
Sequence 15, Appli
Sequence 27, Appl
Sequence 27, Appli
Sequence 89, Appli
Sequence 89, Appli
Sequence 89, Appli
Sequence 89, Appli
Sequence 804, Appli
Sequence 805, Appli
Sequence 806, Appli
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Gaps

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Indels

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Gaps

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61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVFYCQQYGSSPRTFG 120
                                                                                                                                                   61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
                                                                                                      1 METPAQILIFILLIMLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVRGRYLAWYQQK
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  Length 235;
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Score 666; DB 12;
Pred. No. 2.7e-49;
6; Mismatches 8;
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Pred. No. 1.2e-48;
8; Mismatches 6
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                                                                                                                                                                                                                                 121 OGTRLEIKGTVAAPSVFIFPPS 142
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89.5%;
  90.9%;
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Best Local Similarity 89.5
Matches 128; Conservative
Query Match
Best Local Similarity 90.1
Matches 128; Conservative
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; ORGANISM: Homo sapiens
US-09-859-053-34
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SEQ ID NO 34
LENGTH: 236
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                                                                                                      1 METPAQLLFLLLLMLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQR 60
                                      METPAQLLFLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK 60
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93.0%; Score 682; DB 14; Length 235;
Best Local Similarity 92.3%; Pred. No. 1.1e-50;
Matches 131; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                  Sequence 7, Application US/10153382
Publication No US20030086930A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REPERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR APPLICATION NUMBER: 60/293042
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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Publication No. US2004003353A1

GENERAL INFORMATION:
APPLICANT: Boyle, William J
APPLICANT: Martin, Francis H
APPLICANT: Corvalan, Jose R
APPLICANT: Corvalan, Jose R
APPLICANT: Davis, C. Geoffrey
TILE OP INVENTION: Antibodies to OPGL
FILE REFERENCE: 06843.0049-0000
CURRENT APPLICATION NUMBER: US/10/180,648
CURRENT APPLICATION NUMBER: 60/301,172
PRIOR APPLICATION NUMBER: 60/301,172
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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COGGANISM: Mus musculus
US-10-180-648-4
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US-10-153-382-7
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Sequence 8, Application US/10044569B
Publication No. US20030175268A1
GENERAL INFORMATION:
APPLICANT: D. Collen Research Foundation vzw
APPLICANT: D. acquemin, Marc G
APPLICANT: Saint-Remy, Jean-Marie R
TITLE OF INVENTION: Method and pharmaceutical composition for preventing
TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
FILE REPERBNCE: C1968
CURRENT APPLICATION NUMBER: US/10/044,569B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYXCQQFGSSPMCSF 120
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APPLICANT: TBUJI, Takashi
APPLICANT: TBUJI, Takashi
APPLICANT: TBUJI, Takashi
APPLICANT: TBUJI, Takashi
APPLICANT: TEJAKA, KATSUNATI
APPLICANT: HOAL, NO. USZOOZOIOZESBALUAKI
APPLICANT: HOAL, NO. USZOOZOIOZESBALUAKI
APPLICANT: HOAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HOAN MONOCLONAL SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: PHARVACEUTICAL USE THEREOF
FILE REPERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT APPLICATION NUMBER: US/09/859,053
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
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SEQ ID NO 15
LENGTH: 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGQAPRILIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSA-ITF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PGQAPRILITYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLFF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 METPAQLIFILILIWIPDTTGEIVLTQFPGTLSLSPGERATLSCRASGSVASAYLAWYQQK 60
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CTHER INFORMATION: complementary determining region number three US-10-044-569B-8
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                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (127). (162)
OTHER INFORMATION: complementary determining region number one
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LOCATION: (205)..(225)
OTHER INFORMATION: complementary determining region number
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Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICAMT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE PREPERCE: PC23019A:
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT PILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 89.3%; Score 654.5; DB 14; Best Local Similarity 89.5%; Pred. No. 1.5e-48; Matches 128; Conservative 7; Mismatches 7;
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Pred. No. 2.8e-48;
4; Mismatches 8;
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,405
PRIOR FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity 90.1%;
Matches 128; Conservative
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NAME/KEY: misc_feature
LOCATION: (325)..(354)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 650.5; DB 14; Length 234;
Pred. No. 5.7e-48;
5; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                           Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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US-10-153-382-15
Sequence 15, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PPIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REPERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT APPLICATION NUMBER: 06/293042
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
VUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                                                                                                                                                                         89.2%; Score 653.5; DB 9 89.5%; Pred. No. 3.2e-48; iive 8; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GOGTRLEIKGTVAAPSVFIFPPS 142
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Best Local Similarity 89.4%;
Matches 127; Conservative 5
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Best Local Similarity 89.55
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-10-153-382-15
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-09-859-053-38
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IION: (80) Representation of the maturally occurring L-amino acids a INFORMATION: Xaa equals any of the naturally occurring L-amino acids a YKRY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (71)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEXPAQLIFLILIMIPDITGEIVITGSPXTISISPGERATISCRASGSV-SSYLAWYQQK 59
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Best Local Similarity 84.7%; Pred. No. 1.1e-43;
Matches 122; Conservative 3; Mismatches 16; Indels 3;
                                                                                                                                                                                                       Sequence 237, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TILLE OF INVENTION: Albumin Fusion Proteins
FILE REPERENCE: FF646CT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR PEPLICATION NUMBER: 60/229, 358
PRIOR PELING DATE: 2000-1221
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/296, 384
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-31
PRIOR FILING DATE: 2000-12-51
SRIOR FILING DATE: 2000-12-51
SRIOR FILING DATE: 2000-12-51
SRIOR FILING DATE: 2000-13-51
125 ITFGGGTKVEIKRTVAAPSVFIFPFS 150
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OTHER INFORMATION: Xaa
NAME/KEY: SITE
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INFORMATION: Xaa
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
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Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS HII, THAT
SPECTFICALLY DETECT CANCER CELLS, NUCLEOFIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS---A 116
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                                                                           PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
                                                                                                                            PGQAPRPLIYGVSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCQQYGISPFTFG 119
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           1 METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSV-SSYLAWYQQK 59
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CULTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MOBIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INPORMATION:
NAME: Lehnhardt, Susan K.
REPERENCE/DOCKET NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                            120 PGTKVDIKRTVAAPSVFIFFPS 141
                                                                                                                                                                                                                  121 OGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09782397
Publication No. US20030021779A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
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Best Local Simi
Matches 128;
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PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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US-10-291-265-804
                                                                                                                    121 OGTRLEIK 128
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|20 GGTKVEIK 127
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US-10-291-265-805
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US-10-291-265-804
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US-10-309-764-89

Sequence 89, Application US/10309764

j Publication No. US20030232009A1

j GENERAL INFORMATION:
APPLICANT: Foltz, Ian
APPLICANT: Palathumpat, Aabi
APPLICANT: Palathumpat, Raju
APPLICANT: Palathumpat, Raju
APPLICANT: Ming, Chadwick T.
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
CURRENT APPLICATION NUMBER: US/10/309,764

CURRENT FILING DATE: 2002-12-02
PRIOR FILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 147

SOFTWARE: FASESEQ for Windows Version 4.0
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| Sequence 95. Application US/10309762
| Publication No. US20040018198A1
| GENERAL INFORMATION:
| APPLICANT: Glads, Jean
| APPLICANT: Foltz, Jean
| APPLICANT: Foltz, Jean
| APPLICANT: Foltz, Jean
| APPLICANT: Gallo, Michael
| APPLICANT: Gallo, Michael
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
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| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE: 5007-12-02
| PRIOR PAPLICATION NUMBER: 60/337275
| NUMBER: OF SECIENCE ANTIBODIES AGAINST CARBOXIC ANHYDRASE: FASESEQ for Windows Version 4.0
| SECOTION 955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
81.3%; Score 596; DB 15; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.4e-43;
Matches 114; Conservative 8; Mismatches 6; Indels
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CORGANISM: Homo sapiens
US-10-309-762-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 89

| LENGTH: 128

| TYPE: PRT

| ORGANISM: Homo sapiens

US-10-309-764-89
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Sequence 805.4 Application US/10291265

Sequence 805.4 Application US/10291265

publication No. US20030232054A1

GENERAL INFORMATION:

APPLICANT: Hyeeq, Inc.

APPLICANT: Tang et al

TITLE REPRENCE: 21272-017 (788)

CURRENT APPLICATION NUMBER: US/10/291,265

CURRENT APPLICATION NUMBER: 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-77

PRIOR PILING DATE: 2000-07-17

PRIOR PILING DATE: 2000-07-17

PRIOR PILING DATE: 2000-09-15

PRIOR PILING DATE: 2000-09-15

PRIOR FILING DATE: 2000-09-15
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hyeeq, inc.
APPLICANT: Tang et al
TILLE NEFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT APPLICATION NUMBER: US/10/291,265
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-17
PRIOR PILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR PILING DATE: 2000-07-17
PRIOR PLILING DATE: 2000-09-15
PRIOR PLILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
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61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPDDFAVYCQHYGRS-LTFG 119
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80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels 0
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80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels (
                                                                                                                         Length 384;
                                                                                                                                                         5; Indels
                                                                                                                          Query Match

80.5%; Score 590; DB 15;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5;
; NUMBER OF SEQ ID NOS: 944
; SOFWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 384
; TYPE: PRT
; ORGANISM: HOMO sapiens
US-10-291-265-805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: April 5, 2004, 13:59:13 Job time : 34.3976 secs
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CORGANISM: Homo sapiens
US-10-291-265-806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09472087

Sequence 14, Application US/09472087

Patent No. 668736

GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, BILEN E.
APPLICANT: MUELIER, BILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GLIMAN, STEVEN C.
APPLICANT: GLIMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PPI
CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT FILICATION NUMBER: 06/113,647

PRIOR RILIGATION NUMBER: 06/113,647

RICHARD DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 147

SEQ ID NO 14

LENGTHREE 235

THE SECRETARY OF SEQ ID NOS: 120
US-08-812-586-16
US-09-535-822A-17
US-08-27-8235-822A-17
US-08-899-575-153
US-08-899-577-153
US-09-472-087-21
US-09-472-087-93
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US-08-477-087-92
US-08-477-087-92
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US-09-472-087-65
US-09-472-087-65
Sequence 65, Application US/09472087
Patent No. 6682736
GENERAL INPORMATION
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
         Query Match
Best Local Simi
Matches 131;
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US-09-472-087-14
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Copyright (c) 1993 - 2004 Compugen Ltd
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61 PGQAPRILLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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                                                                                                                                                                                                                         APPLICANT: MUBLIER, BILLEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CONVALAN, JOSE R.

TITLE OF INVENTION HUMAN MONCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PF1

CURRENT APPLICATION NUMBER: 05/9472,087

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 67
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APPLICANT: CORVALMA, JOSE R.
TILLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REPERCE: ABX-PF1
CURRENT APPLICATION NUMBER: U8/09/472,087
CURRENT PILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR PILING DATE: 1998-12-23
NUMBER OF FELING DATE: 1998-12-23
SOFTWARE: PALENTING DATE: 1988-12-23
SOFTWARE: PALENTING DATE: 1988-12-23
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SOFTWARE: PALENTING DATE: 1988-12-23
SOFTWARE: PALENTING DATE: 234
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Pred. No. 4.1e-52;
4; Mismatches 8
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Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, ELLEN E.
APPLICANT: MUSEULE, ELLEN E.
APPLICANT: HANKE, JEFREY H.
APPLICANT: GILAAN, STEVEN C.
APPLICANT: GILAAN, GENERY
APPLICANT: CORVALAN, JOSE R.
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     121 OGTRLEIKGTVAAPSVFIFPPS 142
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Patent No. 6682736
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90.1%;
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
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Best Local Similarity 90.1
Matches 128; Conservative
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CORGANISM: Homo sapiens
US-09-472-087-67
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APPLICANT: MEVEU, MARK J.
APPLICANT: MUSUBLER, ELLLER E.
APPLICANT: MUSUBLER, ELLLER E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GOVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ARK-PF1
CURRENT APPLICATION UNMERR: US/09/472,087
CURRENT APPLICATION NUMBER: 6/113,647
PRIOR APPLICATION NUMBER: 6/113,647
PRIOR PILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
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Pred. No. 4.1e-52;
4; Mismatches 8; Indels
APPLICANT: HANKE, JEFEREY H.
APPLICANT: GALMAN, STEVEN C.
APPLICANT: GALMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFREY
APPLICANT: CORVALAN, JOSE R.
TITLE CO INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PE;
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 65
LENGTH: 235
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Pred. No. 1.2e-54;
6; Mismatches 5; Indels
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Patent No. 6682736
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Best Local Similarity 90.1
Matches 128; Conservative
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CAGANISM: Homo sapiens
US-09-472-087-15
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CRGANISM: Homo sapiens
US-09-472-087-65
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61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS----A 116
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Patent No. 5744585
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Patent No. 5744
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                                                                                                                                                                                                               STATE: ....
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFTCATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
NAME: Lehnhardt, Susan K.
RECISTRATION NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
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87.7%; Pred. No. 7.1e-52;
Live 6; Mismatches 8;
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8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 ITFGOGTRLEIKGTVAAPSVFIFPPS 142
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                        NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STRET; 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: WISCOUNTRY: USA
COUNTRY: USA
ZIP. 3717-1914
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.77
Matches 128; Conservative
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                                                                             Query Match 88.7%; Score 650.5; DB 4; Length 234; Best Local Similarity 89.4%; Pred. No. 8.6e-52; Matches 127; Conservative 5; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.7%; Score 650.5; DB 4; Length 234; 89.4%; Pred. No. 8.6e-52; ive 5; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 69. Application US/09472087

Sequence 69. Application US/09472087

Seneral No. 6682736

GENERAL INPORMATION:
APPLICANT: HANGEN, DOUGLAS C.
APPLICANT: HANGEN, BILEN E.
APPLICANT: GILAN, JEFREY H.
APPLICANT: GILAN, JOSE R.
APPLICANT: GILAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PP1
CURRENT APPLICATION NUMBER. US/09/472,087

CURRENT APPLICATION NUMBER: 05/09/472,087

CURRENT FILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ 1D NOS: 147

SOFTWARE: PATENTIN NOS: 147

SOFTWARE: PATENTIN NOS: 147
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Patent No. 6207153
GENERAL INFORMATION:
APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
ITILE OF INVENTION: ANTIGEN BINDIP
ITILE OF INVENTION: FREGMENTS, ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.4
Matches 127; Conservative
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US-09-472-087-69
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US-09-472-087-69
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US-09-472-087-17
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61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRVEPEDFAVYXCQQYDNSVCTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METPAQLIFLILIMIPDITGEIVLTQSPGTLSLSAGERATLSCRASQSVSSRYLAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLIFLILIMIPDITGEIALIQSPGTLSLSPGERATLSCRASOSFSSSYLAWYQQK
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Fatent No. 5661016
GENERAL INFORMATION
THORMATION
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townseend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 105A
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
CMPUTER: IBM PC compatible
CMPTUTER: IBM PC compatible
CMPTUTER: BATENIT Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-ARR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 10-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 10-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: 10-MAR-1992
ATTORNEY AGENT INFORMATION:
NAME: SMICH: WILLIAM M:
REGISTRATION NUMBER: 14643-9-3
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.1%; Score 602; DB 2; L. Best Local Similarity 90.6%; Pred. No. 1.1e-47; Matches 116; Conservative 4; Mismatches 8;
                    REFERENCE/DOCKET NUMBER: 4145C
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-3400
TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 QGTRLEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QGTKLEIK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PGQAPSLLIYGASTRATGIPDRFSGSGSGTDFILTISRLEFEDFAVYCQQYGSSARYTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 METPAQLIFILILMLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSFSRSFLAWYQQK 60
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 624.5; DB 1;
Pred. No. 1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                    CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/POCKET NUMBER: 34656.009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2106
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08480774A Patent No. 5852186 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.8%;
Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 134 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-480-774A-4
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LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
US-08-096-762-183
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 METPAQLLFLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGQAPRILITYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 183, Application US/08096762
Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonbergy, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                        Ouery Match 78.3%; Score 574; DB 1; Length 116; Best Local Similarity 95.7%; Pred. No. 3.4e-45; Matches 110; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 200 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUDNIKK: USAN

ZUP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOUTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-UL-1993
CLASSIFICATION NUMBER: US 07/990,860
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 25-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 13-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 13-JUN-1992
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 13-JUN-1992
ATTORNEY/AGENT INPORMATION:
NAMME: SMEICH WILLIAM M.
REGISTRATION NUMBER: 14643-9-4
TELECOMMUNICATION INPORMATION:
NAMME: SMEICH WILLIAM M.
REGISTRATION NUMBER: 14643-9-4
TELESCOMMUNICATION INPORMATION:
TELEBRANCE/DOCKET NUMBER: 14643-9-4
TELEBRANCE/DOCKET NUMBER: 14643-9-4
TELEBRANCE/DOCKET NUMBER: 1893:
SEQUENCE CHARACTERISTICS:
                               TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
                                                                                                                                                               TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-053-131-183
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TTTE: amino acid

NOMECURY TYPE: Procest

Base: Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Reach Local Similarity 95-71; Fred, No. 3.44-45;

Result 12

Result 12

Result 12

Result 12

Result 12

Result 12

Result 13

Result
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Query Match
Best Local Similarity 95.7
Matches 110; Conservative
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OGNISM: Homo sapiens
; OTHER INFORMATION: M1-23L
US-09-456-090A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (4119 INFORMATION FOR SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
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ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 3.4e-45;
3; Mismatches 2
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APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
              FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 10-OCT-1995
FILING DATE: 10-OCT-1995
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
ATTORNEY,AGENT INPORMATION:
US 08/209,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 311, Application US/08758417A Patent No. 6300129 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0.14
TELECOMMUNICATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.7%;
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS: LENGTH: 116 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-09-042-353-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Garay, Jeff
APPLICANT: Caray, Jeff
APPLICANT: Londberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERRNCE: 020015-00020005
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARR: Patentin Ver. 2.1
SSG ID NO 50
LENGTH: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.3%; Score 574; DB 4;
95.7%; Pred. No. 3.4e-45;
tive 3; Mismatches 2
                                                                                                                                                                                           APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
APPLICATION NUMBER: US 08/096,762
APPLICATION NUMBER: US 08/096,762
APPLICATION NUMBER: US 08/095,762
                                                   APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/352,322
APPLICATION NUMBER: US 08/209,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 08/728,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
MOLECULE TYPE: procein
; SEQUENCE DESCRIPTION: SEQ ID NO: 311:
US-08-758-417A-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 50, Application US/09456090A; Patent No. 6680209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120
                                                                                                                                                  81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS-AITFGQGTRLEIKGTVAAPSVFIF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 BIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIP 80
                                                                                                21 BIALTOSPGTLSLSPGERATLSCRASOSFSSSYLAWYQOKPGQAPRLLIYGASTRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 573.5; DB 4; Length 226;
Pred. No. 8.2e-45;
4; Mismatches 5; Indels 1; Gaps
                                        Gaps
                                        1;
                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-456-090A-86

Sequence 86, Application US/09456090A

Patent No. 6680209

GENERAL INFORMATION:

APPLICANT: Buchler, Joe

APPLICANT: Gray, Jeff

APPLICANT: Colberg, Nils

APPLICANT: Lonberg, Nils

TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS

FILE REFERENCE: 020015-000200US

CURRENT FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 110

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 86

LENGTH: 226

TYPE: PRT

ORGANISM: Homo sapiens

OTGANISM: Homo sapiens

US-09-456-090A-86
Query Match 78.2%; Score 573.5; DB 4; Length 226; Best Local Similarity 91.9%; Pred. No. 8.2e-45; Matches 113; Conservative 4; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.9%;
Matches 113; Conservative 6
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5, 2004, 13:44:08

Search completed: April Job time: 12,7343 secs

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April 5, 2004, 13:25:01; Search time 12.6701 Seconds (without alignments) 1184.358 Million cell updates/sec
                                                                                                                                                                                US-10-044-569B-6
837
1 MDWTWRILFLVAAATGAHSQ......GYTSHYFDYWGRGTLVTVSS 156
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                            283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	anti-Sm a	neavy chain V	chain V	neavy chain V	neavy	neavy chain V	neavy	i-PR2 erythr	heavy	heavy	heavy chain	heavy	heavy	heavy	heavy chain		mu chain pre	heavy chain	heavy	heavy chain	heavy chain	gamma chain	heavy chain	heavy	heavy chain	Ig heavy chain pre	heavy	heavy chain	Ig heavy chain pre
	ID	953	S23623	S18551	S31600	HVHU35	831680	831596	PL0105	829257	S19245	846393	D33548	A32483	S18553	S21916	S36265	S14683	HVHUHG	E1HUND	S18552	821924	PT0371	MHMS18	C41287	S18554	HVMST7	869899	PH1669	A30577
	DB	2	~	N	N	Н	7	0	N	7	N	N	~	N	Ŋ	~	N	N	Н	Н	01	7	N	Н	7	C7	Н	N	(1	N
	Vuery Match Length	; -	171	117	136	117	117	132	160	148	142	129	123	142	117	134	118	627	117	143	117	131	117	139	137	117	138	104	110	135
ar (Match	2 .	70.7	65.7	65.7	65.5	64.5	62.5	62.2	61.8	61.5	60.3	60.0	59.5	58.9	58.7	58.6	58,4	58.1	57.6	57.0	56.6	55.6	55.5	55.3	55.0	54.5	54.2	54.2	53.8
		ເເດ	591.5	550	549.5	548	540	523.5	521	517	515	505	502	498	493	491	490.5	489	486	482.5	477	474	465	464.5	462.5	460	456	454	453.5	
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Ig heavy chain pre To heavy chain V r	heavy	heavy	heavy	heavy	heavy	heavy	heavy	gamma	heavy chain	heavy	heavy chain	heavy chain		Ig gamma-2a chain
E32513	S26938	\$20783	G2MS43	831698	826912	PH1668	F29380	G2MS11	S31667	H32513	S34014	I44151	五29380	537483
010	10	7	rH	~	~	7	(1	٦	N	(1)	N	N	ď	6
138	1 86	121	137	116	86	109	137	474	116	137	127	126	137	469
53.8	53.4	52.9	52.5	52.4	52.3	52.3	52.3	52.3	52.2	52.0	52.0	51.9	51.8	51.8
450	446	443	439.5	438.5	438	438	437.5	437.5	436.5	435.5	435	434	433.5	433.5
30	32	8	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

Aspesson antibody VH chain (VHI/DKI or DMI/JH4b) - human cistories: Homo sapiens (man) C;5Deceies: Homo sapiens (man) C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999 C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999 C;Accession: S49530 R;Andmoudd, M:; Edwards, J:; Cairns, E.; Bell, D. S;Andmoudd, M:; Edwards, J:; Cairns, C.; Bell, D. S;Andmoudd: Molecular characterization of natural human anti-Sm autoantibodies. A;Description: Molecular characterization of natural human anti-Sm autoantibodies. A;Accession: S49530 A;Accession: S49530 A;Accession: S49530 A;Accession: S49530 A;Accession: S49530 A;Accession: MRNA A;Residues: 1-135 - MAH> A;Residues: 1-135 - MAH> C;Superfamily: immunoglobulin V region; Immunoglobulin homology	Ouery Match 72.5%; Score 606.5; DB 2; Length 135; Best Local Similarity 77.6%; Pred. No. 4.99-46; Matches 121; Conservative 6; Mismatches 8; Indels 21; Gaps 3; Qy	QY 61 YSVHWVRQAPGQGLEMMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120 Db 51 YYMHWVRQAPGQGLEMMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDT 110 QY 121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156 Db 111 AVYYCARARTGYNYWGQGTLVTVSS 135	RESULT 2 S23623 Ig heavy chain V region precursor - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999 C;Accession: 623623 R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Mae(175, 831-842, 1992 A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from A;Reference number: 823623; MUID:92156804; PMID:1740665 A;Accession: 823623 A;Accession: 823623 A;Status: preliminary A;Residues: 1-171 cOLES A;Residues: 1-171 cOLES A;Cross-references: EMBL:X59702; NID:932010; PIDN:CAA42223.1; PID:932011 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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Igheavy chain precursor V region (V35) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C;Accession: 800476; $34013
R;Mateuda, P:; Lee, X.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuh
EMBO J. 7, 1047-1051, 1988
A;Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain l
A;Reference number: $00476; MUID:88296408; PMID:2841108
A;Accession: $00476
A;Molecule type: DNA
A;Residues: 1-117 <AATS>
A;Residues: EMBL:X07448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
A;Note: the authors translated the codon AGT for residue 89 as Met
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
B;Mr. J: Immunol. 23, 846-851, 1993
A;Accession: S34001; MUID:93209281; PMID:7681398
A;Accession: S340013
A;Accession: S340013
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: S31585
A; Reference number: S31585
A; Reference number: S31600
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-136 < CUI>
A; Cross-references: EMBL: Z14165; NID: 930994; PIDN: CAA78534.1; PID: 930995
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology < IMM>
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A,Introns: 16/1
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;1-13/Domain: signal sequence #sterus predicted <8IG>
F;1-13/Domain: signal sequence #sterus predicted <8IG>
F;2-117/Product: Ig heavy chain V region (V35) #status predicted ·
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                   Length 136;
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Pred. No. 5.4e-41;
4; Mismatches B;
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                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                65.7%; Score 549.5; DB 2
69.9%; Pred. No. 4.7e-41;
ive 12; Mismatches 14
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A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
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larity 82.7%;
Conservative
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Best Local Similarity 69.9%
Matches 109; Conservative
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A;Molecule type: mRNA
A;Residues: 20-116 <MAR>
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les 105; Conserv
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: 818551; 823625
R;Shin, E.X.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H. Rishin, E.X.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H. A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl. A;Reference number: 818551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ajmolecule type: DNA
AjResidues: 1-17 <SHI.>
Ajross-trences: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
Ajcross-tripu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
Ajritle: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the Ajreference number: S23623; MUID:92156804; PMID:1740665
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31600
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
                                                                                                                                                                                                                           1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKGSGYT-----FTA
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                                                                     Length 171;
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                                                                                                                         Indels
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Pred. No. 1.3e-44;
9; Mismatches 19;
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                 immunoglobulin homology <IMM>
                                                                        70.7%;
75.0%;
                                                                                                                              Conservative
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                                                            Query Match
Best Local Similarity
Matches 117; Conserv
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                    F;34-117/Domain:
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S29257.

S29257.

S29257.

Ig heavy chain V region precursor - human (fragment)

C)Species 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C)Bate: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C)Accession: S29257

C)Accession: S29257

A)Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment

A)Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment

A)A.Pitle: Molecular characterization of A)Accession: S29257

A)Actures preliminary

A)Acture DAA

A)Acture
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51 YDIDWVRQATGGGLEWMGHMNPNSGNTGYAQKFQGRVTWTRNTSISTAXMELSSLRAEDT 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
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R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
A; Exp. Med. 169, 1631-1643, 1980
A;Title: Relationship of variable region genes expressed
A;Réference number: PL0106; MUID:89235583; PMID:2541221
A;Accession: PL0105
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Best Local Similarity 65.4%; Pred. No. 3.5e-38;
Matches 104; Conservative 15; Mismatches 26;
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Pred. No. 1.7e-38;
8; Mismatches 30;
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Best Local Similarity 67.9%;
Matches 106; Conservative
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Cipecies: Homo sapiens (man)
Cipate: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Cidecesion: S1680
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Reference number: S1585
A;Accession: S1680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <CUI.>
A;Cross-references: EMBL:Z14213; NID:g37795; PIDN:ChA78582.1; PID:g37796
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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Pred. No. 2.7e-40;
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Best Local Similarity 81.1%; Pred. No. 2.7e-
Matches 103; Conservative 7; Mismatches
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| AVYYCAR 117
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Jacob Ready chain V region - human (fragment)

Ly heavy chain V region - human (fragment)

Cybaces: Homo sapiens (man)

Cybaces: 12-Oct.1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996

Cybacesion: A32483

Ry Larrick, Jw.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989

Ay Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells us A, Reference number: A32483

A, Reference number: A32483

A, Accession: A32483

A, Accession: A12483

A, Residues: 1-142 cLAR>
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C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Steywords: heterotetramer; immunoglobulin
F.15-98/Domain: immunoglobulin homology <IMM'>
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig neavy chain V-1 region (WIL2) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 17-Jan-1990 #text_change 16-Aug-1996 C;Accession: D33548 P;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A. Proc. Natl.: Acad. Sci. U.S.A. 86, S913-5917, 1995 A;Title: Developmentally restricted immunoglobulin heavy chain variable region shacemence number: A33548; MUID:89345575; PMID:2503826 A;Starus control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
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                                                                          INPNSGATDYAHKEQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
                                                                                                                        51 INPNSGGTNYAQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYDSSGYY 110
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C,Superfantly: immunoglobulin v region; immunoglobulin homology
C,Keywords: heteroferamer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>
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59.5%; Score 498; DB 2; L
Best Local Similarity 67.8%; Pred. No. 1.5e-36;
Matches 103; Conservative 10; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%; Score 502; DB 2;
ilarity 72.5%; Pred. No. 5.9e-37;
Conservative 10; Mismatches 12.
        1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTG-
                                                                                                                                                                                                                                    140 S--HYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| |||||:|||||||
106 CYYFFDYWGQGTLVTVSS 123
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                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 100; Conserv
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(Species: Homo sapiens (man)

(Species: Homo sapiens (man)

(SACCESSION: S19245

R;Kirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.

EMBO J. 11, 603-609, 1992

A;Title: Immunoglobulin V(H) clan and family identity predicts variable domain structure

A;Title: Immunoglobulin V(H) clan and family identity predicts variable domain structure

A;Reference number: S19245; MUID:92164649; PM(ID:1537339

A;Reference prediminary; translation not shown

A;References: DNA

A;Residues: 1-142 <RIR>
A;Cross-references: EMBL:X59906; NID:g37791; PIDN:CAA42547.1; PID:g37792

A;Cross-references: EMBL:X5900blin V region; immunoglobulin homology

C;Superfamily: immunoglobulin homology <IMM>

F;34-117/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Cession: 846393
R;Figini, M: Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Reference number: 846390; MUID:94254092; PMID:8196048
A;Accession: 846393
A;Accession: breliminary
A;Residues: 1-129 <FIG>
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Pred. No. 3.4e-37;
8; Mismatches 18; Indels
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                                                 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYT-
                                                                                                                                                                                                                                                                                      121 AMYYCARADNYFDIVTGY---TSHYFDYWGRGTLVTVSS 156
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Best Local Similarity 72.7%;
Matches 101; Conservative
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Length 134; Indels

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51 YALNWIRQAPGGGLEMMGHINTNIGKATYAQAFIGRFVFSLDISVSTTYLQISSLKAEDT 110
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C;Keyword8: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <81G>
F;20-134/Product: Ig heavy chain V region (fragment) #status predicted <WAT>
F;34-117/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                             1 MDWTWRILFLVAAATGAHSQVQLIQSGSELRKPGASVKVSCKASGYTFTN-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
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Best Local Similarity 59.6%; Pred. No. 5.9e-36;
Matches 93; Conservative 19; Mismatches 22
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NyAlternate names: rheumatoid factor
NyAlternate names: rheumatoid factor
C;Becies: Homo sapiens (man)
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 21-Jan-2000
C;Accession: S21916
K;Mierau, R.; Gause, A.; Kueppers, R.; Michels, M.; Mageed, R.A.; Jefferis, R.; Genth, E submitted to the EMBL Data Library, July 1991
A;Description: A Human monoclonal IgA rheumatoid factor using the Vk(IV) light chain gen
                                                                                                                                                                                                                                                                                                                                                                                     R;Shin, Ext.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl A;Reference number: S18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1.17 <-SHI>
A; Residues: EMBL:X62109
A; Cross-references: EMBL:X62109
B; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A; Thitle: The repertoire of human germline V(H) sequences reveals about fifty groups of A; Reference number: $26885, MUID:93021117; PMID:1404388
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                PGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCAR-- 127
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                                                                                                                                                                                                                                                                                                                         Species: Homo sapiens (man)
Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
Accession: S18553; S26916
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                              heavy chain V region precursor (VI-3b) - human (fragment)
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                                                                                                               128 -ADNYFD--IVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                Accession: S18553
Status: translation not shown
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| AVYYCAR 117
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A, Residues: 20-117 < TOM>
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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 5, 2004, 12:10:21; Search time 7.1269 Seconds (without alignments) 1139.758 Million cell updates/sec Run on:

US-10-044-569B-6 837 1 MDWTWRILFLVAAATGAHSQ......GYTSHYFDYWGRGTLVTVSS 156 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P23083 homo sapien	13 homo	ม ธกม	30 mus	Sp mus	16 mus	99 mus	3 mus	18 mus	o mus	S mus	mus	mus /	mus	8 mus	Bru	EUM.	7 mus	EUI	พกร พ	6 homo	2 нопо	พนธา	mus m	homo	рошоц	homo	แนย ก	rattu	01761 homo	1808 mus	P01807 mus musculu
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HV07 MOUSE
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        61 YSVHWVRQAPGGGLEWMGRINPNSGATDYAHKFOGRVTMSRDTSISTAYMELSRLTSDDT 120
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Immediate hypersensitivity: modern concepts and developments, pp.1-36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL_1986 (Rel. 01, Created)
LoCT-2001 (Rel. 40, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-I region ND precursor (Fragments).
Enhancy splans (Human).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marcel Dekker, New York (1978).
-!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:006555; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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(WH) gene subgroups...;
Proc. Nacl. Acad. Sci. U.S.A. 80:855-859(1983).

Proc. Nacl. Acad. Sci. U.S.A. 80:855-859(1983).

Proc. Nacl. Acad. Sci. U.S.A. 80:855-859(1983).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                          MEDLINE-83144028; PubMed=6298778; Rechavi G., Ram D., Glazer L., Zakut R., Givol D.; "Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                          Eukaryoča, Meražoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 486; DB 1; Length 117; Pred. No. 1.1e-40; 9; Mismatches 16; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V-I REGION HG3 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 117
117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
                                                    21-JUJ-1986 (Rel. 01, Created)
21-JUJ-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 havy chain V-I region HG3 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV07_MOUSE STANDARD; PRT; 139 AA P01751; P01752; P01752; P01752; P01751; P01752; P01701-1986 (Rel. 01, Last sequence update)
117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005955; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00047, ig, 1.
SMARY, SM00406, iGv. 1.
PROSITE, PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.1%;
72.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J00240; AAA52988.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92; Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
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Best Local Similarity
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YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKRQGRVTMSRDTSISTAYMELSRLTSDDT 120
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"Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).
-i- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGWSYIILFLVATATDVHSQVQLQQPGAELVKPGASVQLSCK------ASGHTFTN
                                                                                                                                                        WEDLINE=84248078; PubMed=6429663;
Silliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                           "Illegitimate recombination generates a class switch from C mu to delta in an IgD-secreting plasmacytoma.";
PINC. Natl. Acad. Sci. U.S.A. 81:4164-4168 (1984).
PIN. Ac2033; HYMST7.
HSSP, PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
FRO047; ig; 1.
SMART; SM00406; iGV.
IMMART; PS000405; iGV.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION TEPC 1017.
PRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%; Score 456; DB 1; Length 138; 55.8%; Pred. No. 1.1e-37; Live 23; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15576 MW; 748157E4C6907B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVYYCARSDGYYD------WFVYWGQGTLVTFSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-UU-1986 (Rel. 01, Created)
21-UU-1986 (Rel. 01, Last sequence update)
15-UU-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region S43 precursor.
Mus musculus (Mouse).
15-JUL-1999 (Rel. 38, Last annotation update) Ig heavy chain V region TEPC 1017 precursor. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 AA.
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BY SIMILARITY.
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 AA;
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                   Cucker P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV11 MOUSE
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SEQUENCE
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HV11 MOUSE
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            임
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                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation—the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YWMHWVKQRPGRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDS 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                               MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAVY CHAIN V REGION B1-8/186-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.5%; Score 464.5; DB 1; Length 139; 57.7%; Pred. No. 1.7e-38; ive 20; Mismatches 29; Indels 17.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, J00529; AAA38170.1; -.
PIR; A50809; MHM018.
PDB; 1A6U; 27-MAY-98

IDB; 1A6W; 15-UUL-98.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 1.
PRORIT; RS00406; IGV; IGV; IRE; I.
PRORIT; RS08035; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
  (Rel. 42, Last annotation update)
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(Rel. 02, Last sequence update)
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D SEGMENT.
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FRAMEWORK-1.
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                                                                                                                                                                                                                                                                                                                                            (NPB ANTIBODIES).
                     Ig heavy chain V reg:
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 AA;
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Best Local Similarity
Matches 90; Conserv
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                        Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1986
23-OCT-1986
    10-OCT-2003
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 YLMHWVNQRPGRGLEWIGRIDPNSGGTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSEDS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
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MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Somatic mutation in genes for the variable portion of immunoglobulin heavy chain."; Science 216:309-311(1982).
-! SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15200 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 55.1%; Pred. No. 4.6e-36; tes 86; Conservative 18; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:||||||
| AVYYCARY-----RLGRYFDYWGQGTTLTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.5%; Score 439.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK-3.
D SEGMENT.
                                                                                                                                                                                                                             EMBL, JO0539, AAA38172.1; -...
PIR; AQ2038; G2M843.
HSSP; PO1810; ZFBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PR00047; ig; 1...
PROSITE; MONOG, IG'. 1...
PROSITE; PS50835; IG_LIKE; 1...
IMMINGGlobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 1
137 AA;
                      (NPB ANTIBODIES)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capra J.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P01759;
21-JUL-1986 (Rel. 01, Created)
10-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region BCL1 precursor.
Bukarycta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION 93G7 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15514 MW; 25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.7%; Score 416; DB 1; 50.6%; Pred. No. 9.3e-34; ive 29; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PP00047; ig; 1. "SMARY; SMARY; SP000466; IGV, 1. PR06817; PS06815; IG LIKE; 1. Immunoglobulin V region; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                 PIR, A94264; HVMSG7.
HASRP, PO1810, 2FBJ.
INCEPERO, IPROC110; IG-like.
InterPro, IPRO03596; IG-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J00494; AAA38130.1; -. PIR; A02042; HVMSB1.
                                                                                                                                                                                                                                                       EMBL; J00493; AAA38128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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139
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hes 79; Conserv
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SEQUENCE FROM N.A.
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10; Gaps

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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                       1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYT-----FTS 50
                                   1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
             Indels
  Best Local Similarity 59.8%; Pred. No. 1.8e-32;
Matches 76; Conservative 18; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.6%; Score 398; DB 1;
59.8%; Pred. No. 4.3e-32;
iive 17; Mismatches 24;
                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 23 precursor.
                                                                                                                                                                                                    117 AA.
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                                                                                                                                                                                                    STANDARD;
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                                                                                                                          121 AMYYCAR 127
                                                                                                                                               111 AVYYCAR 117
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50
69
86
81
117
117
AA;
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les 76; Conserv
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P01748;
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SEQUENCE
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                                                                                                                                                                                                                                                1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
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                                                                                                                                                                                                          1 MGWSCIIFFLVATATGVHSQVQLQQSGPEVVRPGVSVXISCKGSGYTFTD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PELATED GENES THAS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

PIR, D90809; HWN561.

HSSP, P018010; ZPBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.

PRAM; PR0047; Ag; 1.

SMAR; SM00406; IGv.

Inmunoglobulin V region; Signal.
                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION 186-1.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                               Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                        IG HEAVY CHAIN V REGION BCL1. IG-LIKE.
                                                                                                                                                                   33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12890 MW; 16191A088CB17F5A CRC64;
                                                                                                                          15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                             111 ANLYCAR-----YYGNYFDYWGQGTTLTVSS 136
                                                                                                                                               49.3%; Score 413; DB 1; 52.6%; Pred. No. 1.8e-33;
                                                                                                                                                                                                                                                                                                                                                          HV09_MOUSE STANDARD; PRT; 117 AA. P01753, P11271; Created) 01-JUL-1986 (Rel. 01, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Mus musculus (Mouse).
                                                                                                                                                                   21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
HSSP; PO1772; 2FB4.
InterPro; IPRO07110; Ig-like.
InterPro; IPRO03596; Ig-v.
Ffam; PPO0047; ig; 1.
SWART; SWO0406; IGv; 1.
PROSITE; PS50855; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                          Query Match
Best Local Similarity 52.6*
Matches 82, Conservative
                                                                                       20 1
20 1
136 AA;
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55
69
86
41
117 AA;
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SEQUENCE
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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                  "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1891).

Cell 24:625-637(1891).

PIST, ANSCELLANBOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

PIR, A02030, HYMS23.

INTERPRO, IPRO07110; 19-1ike.

InterPro, IPRO03190; 19-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGWSCIILFLVAAANGVHSQVQLQQPGTELVKPGASVKLSCKASGYT-----FTS
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                                                                                                                                                                                                                    MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NOSI_TaxID=10090;
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FRAMEWORK-1.
COMPLENENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AVYYCAR 117
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Length 117;

Score 402; DB 1;

48.0%;

Query Match

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121 AMYYCAR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AVYYCTR 117
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[1]
SEOUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV10 MOUSE
P01754; P11270;
21-JUL-1986 (Re
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGWSCIILFLVATATGVHSHVQLQQPGAELVKPGASVKVSCKASGYT-----FTS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                 "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981)
-!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
PIR; A02032; HVMS02.
                                                                                                                                                                              MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN'1988 (Rel. 06, Created)
01-JAN'1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region VHSSB B4 precursor.

Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Musinae,
NCBI_TaxID=10090;
                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.3%; Score 396; DB 1; Length 117; 60.3%; Pred. No. 6.8e-32; ive 17; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN V REGION 102.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              12867 MW; 740A65DD851FCA8C CRC64;
                                                            21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                         117 AA
                                                                                                                                                                                                                                                                          HSS; PO1810; 2FBJ.
Interbro; IPR007110; Ig-like.
Interbro; IPR001359; Ig-v.
Pfam; PF00047; ig; I.
SMART; SM00466; IGv; I.
SMART; SP50835; IG LIKE; I.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity: 60.3%;
les 76; Conservative 1
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                                         STANDARD;
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117
117 AA;
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                                                                                                                                                        SEQUENCE FROM N.A.
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P06328;
                                        HV06 MOUSE
P01750;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 YWMHWVKQRPGRGLEWIGNIDPNSGGTKYNEKFKSKATLIVDKPSSTAYMQLSSLTSBDS 110
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STRAIN=C57BL/6;
STRAINNE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari I., Rajewsky K., Baltimore D.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Heavy chain variable region contribution to the NPb family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V REGION VH558 B4. FRAMEWORK-1.
MEDLINE=85099340; PubMed=2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.5%; Score 381; DB 1; Length 117; 56.7%; Pred. No. 2e-30;
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01-JUL-1989 (Rel. 11, Last sequence update)
19 heavy Chain V region 145 precursor.
1GH-VJ558.
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PIR; A02035; MHMSB4.
HSSP; PO1810; ZFB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
FMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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nes 72; Conservative
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HV50 MOUSE
P06329;
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SEQUENCE
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HV50_MOUSE
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                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eur. J. Immunol. 12:1023-1032(1982).

-!- MISCELLANDOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGWSCIMLFLAATATGVHFQVQLQQPGAELVKPGASVKLSSKASGYT-----FTS
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      antibodies: somatic mutation evident in a gamma 2a variable region.";
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21-UU-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
1110 heavy chain V region 36-65.
1120 heavy chain (Mouse)
1120 heavy chain (Mouse)
1220 heavy chain (Mouse)
1230 heavy chain (Mouse)
1230 heavy chain (Mouse)
1230 heavy chain (Mouse)
1230 heavy chain (Mouse)
1330 heavy chain (Mouse)

                              1 24:625-637(1981).
MISCELLANBOUS: THIS GERMIINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION 145.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.4%; Score 380; DB 1; Length 117; 57.5%; Pred. No. 2.5e-30;
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COMPLEMENTARITY-DETERMINING-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12921 MW; D37DE8A3F543E996 CRC64;
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les 73; Conser
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P01747;
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SEQUENCE
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Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
"Jymbhocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
1g heavy chain V region AC38 15.3.
Ig heavy chain V region AC38 15.3.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 711—TaxID=10090;
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                                                                                                                                                                                                                                                                                                      45.4%; Score 380; DB 1; Length 120;
llarity 53.7%; Pred. No. 2.6e-30;
Conservative 23; Mismatches 24; Indels
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120 AA; 13307 MW; FF04E4A167B654AF CRC64;
     Contains 1 immunoglobulin-like domain
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InterPro; 1PR00710; Ig-like.
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Pfam; PP00047; ig; 1.
SNART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Hybridoma.
DOMAIN.
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---- 73; Conserve
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es 73; Conserv
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Dp ò Search completed: April 5, 2004, 13:24:55 Job time: 7.1269 secs

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

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B chartenton M., Soares M.B., Bonaldo M.F., Caranicol P., Frange C.,

B completion M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B completion M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hales S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hales S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Generation and initial analysis of more than 15,000 full-length human
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Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; EGO51328, AAH51328.1; -.
Hypothetical protein.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO05951; AAH05951.1; -.
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AMYYCARA-DNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 AVYYCARRYCSYSSCONDYYYYYMDVWGKGTTVTVSS 147
                                                                                                                                                                                                                                                                                       60.2%; Score 503.5; DB 4;
65.0%; Pred. No. 1.7e-41;
ive 11; Mismatches 33;
                                                                                                                                   Pfan, PF00047; ig; 4. 5MAFT; SMOATF; SMOATF; SMOATE; PROSITE; PS00290; IG_MHC; 1. PROSITE; PS00290; IG_MHC; 1.
                                                                   Interpro; IPR007110; Ig-like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 65.0%
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC000851; AAH09051.1;
R EMBL; BC000851; AAH09051.1;
R GO; GO:0005622; C:intracellular; IEA.
R GO; GO:000552; C:intracellular; IEA.
R GO; GO:000555; P:transcription of transcription, DNA-dependent; IEA.
R GO; GO:0006355; P:transcription of transcription, DNA-dependent; IEA.
R INTERPO; IPR001005; HTHATA.C.
R INTERPO; IPR001005; IG-MHC.
R INTERPO; IPR003966; IG-WHC.
R SMART; SMO0466; IG-V.
R SMART; SMO0466; IG-V.
R PROSITE; PS00041; HTH AAAC FAMILY_1; 1.
R ROSITE; PS00041; HTH AAAC FAMILY_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.7%; Score 508; DB 4; Length 614; 65.0%; Pred. No. 8.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 614 AA; 67921 MW, SSEF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 TAMYYCARADNYFDIVTGYTSHY---FDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 TAMYYCAR-----GYSSSWDDAFDIWGQGTWVTVSS
                                                            AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
                                                                                                                                                                                                                             Created)
                                                                                                                                                                                    PRT;
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                                                                                                                                                                                    PRELIMINARY;
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Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=B-cell;
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Matches 104;
                                  121
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Q9BRV0;
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159 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P01810, 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
FP00047; ig; l.
SMART; SM00406; IGv; l.
PR0SITE; PS50835; IG_LIKE; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 60.49 hes 96; Conservative
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                PRELIMINARY;
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                         Tilson M.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Q9UL94;
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Q9UL94
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                                                                                                                                                                                             61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                       61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                     20
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A Jacquemin M.G., Vander Elst L.P.L.;
Tacquemin M.G., Vander Elst L.P.L.;
Tacquemin M.G., Vander Elst L.P.L.;
TigG4 monclonal antibody derived from a hemophilia A patient with an inhibitor.";
Elood 92:496-506(1998).
REMBL; AJ224083; CAA11829.1; -..
REMBL; AJ224083; CAA11829.1; -..
RO; GO:0015887; Cintegral to plasma membrane; NAS.
RO; GO:001666; P:cellular defense response (sensu Vertebrata); NAS.
RO; GO:0010666; P:cellular defense response (sensu Vertebrata); NAS.
RITERPRO; IPRO0710; Ig-like.
RITERPRO; PRE003595; Ig_V.
                                                                                                    1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                          Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                 Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.9%; Score 493; DB 4; Length 150; 63.5%; Pred. No. 4e-41; ive 10; Mismatches 27; Indels
                                                                  Indels
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51395 MW; C8D5BE12BAAF795C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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.larity 64.1%; Pred. No. 1.6e-40;
Conservative 13; Mismatches 26;
                                                                                                                                                                                                                                           121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                  PRT; 150 AA.
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IGG VH.
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les 99; Conservative
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150 AA;
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ses 100; Conserv
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Q9Y298

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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Homo saplens putative microfibrillar protein with Ig-like domain 3 mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

MRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AV030025, AAK82649.1; -.

InterPro, IPR00110; Ig-like.

InterPro, IPR00110; Ig-like.

Ffam; PP00047; Ig; I.

SMATT, SMO464; Ig. 1.

SRATT, SMO464; IG. IKE: 1.

SEQUENCE 159 AA; I7497 MW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDWTWRVFCLLAVGPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 AVYFCAREMEITFGGAVSKGFYYYGMDVWGQGTTVTVSS 149
096050;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.5%; Score 489.5; DB 4 60.4%; Pred. No. 9.5e-41; ive 17; Mismatches 33
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Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035020; AAD56256.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
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Homo sapiens
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SIGNAL
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Q96DK0
DATE DE LA PROPERZA LA PRESENTA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 INPNSGGTNYAQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGGRIAA--A 108
                                                                                                                                                                                                                                                                                      80 INPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
                                                                                                                                                                                                                                                                                                                        51 INPNSWTTNYAQKPQKKVTMTKDTSISTAYMELSRLRSDDTAVYYCARG------GGR 102
                                                                                                                                                            79
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                                                                                                                                                            20 OVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR
                                                                                                                                                                                                                  1 EVOLVESGAEVKKPGASVKVSCKASGYTFTG-----YYMHWVRQAPGQGLEWMGW
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                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.9%; Score 476; DB 4; Length 125; 69.3%; Pred. No. 1.5e-39; ive 10; Mismatches 20; Indels
                                 Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 125
125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL. AFO33019; AAD56255.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfan; PR0064; ig; 1.
SMART; SM04406; IGv; 1.
NON TER
125 125
                              56.9%; Score 476; DB 4; 69.3%; Pred. No. 1.4e-39; ive 10; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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MEDLINE=98277139; PubMed=9614934;
MLX., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 SHYFDYWGRGTLVTVSS 156
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095978;
01-MAX-1999 (TREMBLEEL 10,
01-MAX-1999 (TREMBLEEL 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 25,
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                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
   Query Match
Best Local Similarity
....ss 95; Conserve
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Best Local Similarity
Matches 95; Conserv
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01-MAY-2000 (
01-OCT-2003 (
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095978
ID 0959
AC 0959
DT 01-M
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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

TISSUE=Peripheral blood;

TISSUE=Peripheral blood;

TISSUE=Peripheral blood;

DOX A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,

JOX A., Zander T., Wolf J.;

Bohlen H., Diehl V., Wolf J.;

The annuncalboulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated with somatic mutations within the untranslated regions of rearranged and class switch recombinated Ig genes.";

Townstied (APR-1998) to the EMBL/Genbank/DDBJ databases.

EMBL; AJ005570; CAA06599.1;

RICHEPPO; IPR007110; Ig-like.

RICHEPPO; IPR007110; Ig-like.

RICHEPPO; IPR00471; Ig-like.

RICHEPPO; IPR00471; Ig-like.

READ: ARMART; SM00440; Igy.

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EMBL; AKO58027; BAB71633.1; -. Interbro; IPR003106; Ig-Hike.

Interbro; IPR003006; Ig-Hike.

Interbro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDWTWRVFCLLAVAPGVHSQVQLVQSGABIKRPGASVKVHCKTSGY------VFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.8%; Score 475; DB 4; Length 157; 58.3%; Pred. No. 2.6e-39; Artive 20; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 157
157 AA; 17304 MW; 86986EDDA84D8BB5 CRC64;
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01-02C-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ25298
. 25, Last annotation update) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          496 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Conservative
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                                    protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   51 YAFTWYRQAPGQGLQWMGGIIPNFGAPNYAQNFQDRVTISADDSTTTVYMELTSLTFEDT 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR 79
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                                                                                                                                                                                                                                                                                                                                        61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
                                                                                                                                                                                                                                                   1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                         55.7%; Score 466.5; DB 4; Length 496; 59.2%; Pred. No. 8.2e-38; ive 18; Mismatches 31; Indels 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                 SMART; SM00406; TGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00909; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 496 AA; 53532 MW; C72EB1E247C86FED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AMYYCARADNYFDIVTGYTSHYF-DYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFYYCGRGLTYY----GSGSYYYLQHWGQGTLVTVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.9%; Score 459.5; DB 4
66.4%; Pred. No. 6.6e-38;
iive 12; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035022; AAD56258.1; -.
EMSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IRR03596; Ig.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AA.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                            Best Local Similarity 59.2%;
Matches 93; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 66.48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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NETALIZED SOURCE FROM N.A.

SEQUENCE FROM N.A.

NEDINE=2108560; PubMed=11217851;

KRANI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Caarvant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Caarvant T.,

Rochrim L.M., Scaubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Brownstein M.J., Bult C., Pletcher C., Pulita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima N., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima M., Rodriguez I., Sakamacco N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hayashizaki Y.,

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEGUI, PP00017; 1g; 3.
SWART; SW00406; IGY; 1.
PROSITE; PS50385; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 1.
SEQUENCE 473 AA; 51699 WW; 9DED57A514475FBB CRC64;
                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0921K1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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473 AA.
                                                                                 Created)
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PIR, S26746; S26746.
HSSP; P01842; 7FAB.
INCEPPO; 196443; 1gh-1.
InterPro; 1PR007110; 1g-11ke.
InterPro; 1PR003006; 1g_MHC.
InterPro; 1PR003006; 1g_WHC.
                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 54.5
Les 85; Conservative
    PRELIMINARY;
                                                                                                                                                                                                  1810060009Rik protein.
IGH-1 OR 1810060009RIK.
Mus musculus (Mouse).
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Q921K1
ID Q921K
AC Q921K
DT 01-DE
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Search completed: April 5, 2004, 13:42:06 Job time : 34.2589 secs
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                                                                                                                    Q8VCX7
                                                                                                                                     Q8VCX7
                                                                                          RESULT 15
QBVCX7
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                                                                                                                                                                                                                                                                                                                                                                                           61 YSVHWVRQAPGQGLEWMGRINPNSGAIDYAHKFQGRVTMSRDISISTAYMELSRLISDDT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similar to RIKEN cDNA 1810060009 gene.

Was musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                             . Match 54.7%; Score 457.5; DB 11; Length 278; Local Similarity 57.7%; Pred. No. 3e-37; Loss 90; Conservative 16; Mismatches 33; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Straubberg R.,
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888, AAH03888.1; -.
HSSP; P01842; FRB.
InterPro; IPR070110; Ig-like.
InterPro; IPR07013806; Ig-w.
InterPro; IPR003396; Ig-v.
Ffam; PF00047; ig; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS00839; IG-IKE; 4.
PROSITE; PS00839; IG-IKE; 4.
PROSITE; PS00830; IG-IKE; 4.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.2%; Score 445.5; DB 11; Length 52.6%; Pred. No. 9.5e-36; ive 27; Mismatches 34; Indels
                                                                                                       Strausberg R.;
Strausberg R.;
Submitted (ADG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO12207; AAH12207.1; -..
Interpro; IPR007110; Ig-like.
Interpro; IPR007356; Ig-v.
Ffam; PF00047; Ig; 2.
SMART; SM00406; ICv; 1.
PROSITE; PS500835; IG-LIKE; 2.
HYPOCHECICAL protein.
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99L25 PRELIMINARY; PRT; 473 AA.
099L25; CHARBLED 17, Created)
01-JUN-2001 (TEMBLED 17, Last sequence update)
01-JUN-2003 (TEMBLED 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AVYYCTRGYGYDDV-----YFDVWGAGTTVTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82; Conservative
             Hypothetical protein.
Mus musculus (Mouse).
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Best Local Similarity
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                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                              Query Match
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Matches
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Q99L25
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51 HTIHWVKQRPEQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDS 110
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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53.8%; Pred. No. 1.7e-35;
cive 22; Mismatches 31; Indels
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TISSUBE-SAINARY Gland;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
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Last annotation update)
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                                                                                                                                                                                                      121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS
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MGD, MG1:96448; Igh-6.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WPC.
Pfam; PF00047; ig; 5.
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PROSITE, PS50835, IG_LIKE, 5.
PROSITE, PS00290, IG_MHC, 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
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April 5, 2004, 12:09:21 ; Search time 50.4162 Seconds (without alignments) 874 270 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                               - protein search, using sw model
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1586107 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

A Geneseq_29Jan04:*

11: geneseqp1980s:*

22: geneseqp1990s:*

43: geneseqp2001s:*

53: geneseqp2001s:*

64: geneseqp2003s:*

77: geneseqp2003bs:*

88: geneseqp2003bs:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aab47059 Heavy cha
Aac18878 Human KRI
Ade28427 Human ant
Aab52841 Human ant
Aab56215 Human imm
Aay62296 Human imm
Aab57367 Anti-TRAI
Aab57367 Anti-TRAI
Aab57367 Anti-TRAI
Aab57367 Human IGF
Abp45711 Human Col
Aav88464 Monoclona
Aay11804 Monoclona
Aay11804 Monoclona
Aay80299 Humanised
Aay80299 Humanised
Aay80299 Humanised
Aay80299 Humanised
Aay24372 Human BLy
Aar27051 Reshaped
Aaw62204 Humanised
Aaw624371 Humanised
Aaw624371 Humanised
Aaw624371 Humanised Description SUMMARIES AAU74296 AAW22841 AAB53510 AAU31804 ABP45629 Length Query Score Result No.

0 44 0	Aaw46650 Heavy cha Aay96299 Human IGF Abp43131 Human Ova Abp45624 Human BLY		Aar77615 Humanised Aay80288 Humanised Aay02571 Humanised Abp45718 Human BLY	Adw62202 Humanised Adw62202 Humanised Ady02568 Humanised Ady02568 Humanised Ady02572 Humanised
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				4 4 4 4 4

ALIGNMENTS

Monoclonal antibody, variable region, heavy chain, light chain, VH; VL; complementarity determining region; CDR; MAb; BO2C11; conformational epitope, factor VIII; KRIX1; von Willebrand factor; hemostasis; intravascular coagulation; arterial thrombosis; arterial restenosis; venous thrombosis; arteriosclerosis. Heavy chain variable region VH of KRIX1. Location/Qualifiers AAB47059 standard; protein; 156 AA 42. .64 /label= CDR1 79. .95 /label= CDR2 128. .145 /label= CDR3 (first entry) WO200104269-A1. Homo sapiens 08-MAY-2001 18-JAN-2001 AAB47059 Key Domain Domain Domain RESULT 1

13-JUL-2000; 2000WO-EP006677. 99GB-00016450. 99US-0143891P. Jacquemin MG, Saint-Remy JR; (LEUV-) LEUVEN RES & DEV VZW 14-JUL-1999; 14-JUL-1999;

Novel cell lines for producing monoclonal antibodies that bind to a factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders. WPI; 2001-138333/14. N-PSDB; AAC85452.

Example 5; Fig 8; 55pp; English.

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This sequence represents the heavy chain variable region of the monoclonal antibody (MAD), KRIXI. This MAD produced by the cell line of the invention, specifically recognises the wild type factor VIII light chain. KRIXI can be used to inhibit the binding of factor VIII light willebrand factor in a dose dependant manner. The new cell line KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder or thrombotic pathologic condition such as intravascular coagulation, arterial thrombosis, arterial cestencies, venous thrombosis or arteriosclerosis, and attendant of coagulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, antibody; BO2C11; KRIXI; light chain; heavy chain; inflammation; variable region; factor VIII inhibitor; sepsis; septic shock; thrombus formation; systemic inflammatory response syndrome; CDR, disseminated intravascular coaqulation; haemophilia A; immunosuppressive; complementarity determining region; antibacterial; antinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                               YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                              ; Score 837; DB 4; Length 156;
; Pred. No. 3.7e-71;
0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO18878 standard; protein; 156
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 156; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42. .64
/label= CDR1
79. .95
/label= CDR2
128. .145
/label= CDR3
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                                                                                                                                                                                                                                                                      Sequence 156 AA;
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(COLL-) COLLEN RES FOUND VZW D.

WPI; 2002-610270/66

Jacquemin MG,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
                                                                                                                                                The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic Inflammatory response syndrome (SIRS), sepsis, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an extive ingredient a partial inhibitor of factor VIII, in admixture with a carrier. Such inhibitors may include the antibodies B02CII and KRIXI. The present sequence is the heavy chain variable region of KRIXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                Pharmaceutical composition for treating systemic inflammatory response syndrome, sepsis, septic shock and/or thrombus formation in mimmals, comprises a partial inhibitor of factor
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                                                                                                                                                                                                                                                                                                                         Length 156;
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                                                                                                                                                                                                                                                                                                                      100.0%; Score 837; DB 5;
llarity 100.0%; Pred. No. 3.7e-71;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corvalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä.
                                                                                                                    Disclosure, Fig 12; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE28427 standard; protein; 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PFIZ ) PFIZER PROD INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bedian V, Gladue RP,
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 156; Conserv
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N-PSDB; AAL49256
                                                                                                                                                                                                                                                                                          Sequence 156 AA;
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody variable region heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                        Score 611.5; DB 7
Pred. No. 2.8e-49;
7; Mismatches 18
                      Claim 1; SEQ ID NO 34; 177pp; English
                                                                                                                                                                                                                                                                                                                                                                                          73.1%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 76.9
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                              Sequence 471 AA;
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YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120 20 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTG-----Gaps Indels 11; Length 471; 18; 121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156 AVYYCAR-DOPLGYCTNGVCSYFDYWGQGTLVTVSS 145 DB 7; d ઠ 셤 ò g ò

antiallergic; antiuleer; metroprotective; antithyroid; vacotropic; immunosuppressive; dermatological; antinflammatory; hepatotropic; activation inducible lymphocyte immunomodilatory molecule; AllIM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; graft versus host reaction; immune rejection; intelammation; ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis. Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; Anti-human AILIM monoclonal antibody clone Jmab-136, heavy chain. AAU74296 standard; protein; 470 AA. (first entry) 12-MAR-2002 AAU74296;

Homo sapiens.

WO200187981-A2.

22-NOV-2001

18-MAY-2000; 2000JP-00147116. 30-MAR-2001; 2001JP-00099508.

15-MAY-2001; 2001WO-JP004035

(NISB) JAPAN TOBACCO INC.

Hori N;

Isuji I, Tezuka K,

WPI; 2002-075313/10. N-PSDB; AAS99472.

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The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells (I) is useful for treating or prophylaxis of delayed type allergy. (I) is useful for treating and prevention, and for inhibiting the onset and/or advancement of the prophylaxis of delayed type allergy. (I) is useful for treating or transduction, and for inhibiting the onset and/or advancement of the cheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, poortasis, autoimmune or allergic disorders, inflammatory dermatosis, poortasis, autoimmune or allergic disorders, inflammatory dermatosis, poortasis, autoimmune or allergic disorders, inflammatory dermatosis, caused by abnormal intestinal immunity, specifically inflammatory contacting disorders understained disorders such as ulcerative colitis, pneumonia, hepatitis, and pancreative colitis, pneumonia, hepatitis, and pancreative colitis, pneumonia, hepatitis, and pancreative colitis, pneumonia, hepatitis, and minipenicity to human, i.e., human anti-mouse antigenicity (HAMA) in a host. AAU743301 represent anti-human anti-mouse antigenicity (HAMA) in a host. Adva043301 represent anti-human
New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid
                                        lymphocyte immunomodulatory molecule, useful fo
arthritis, multiple sclerosis and inflammation.
                                                                                                                                             Claim 30, Page 264-266; 300pp; English.
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Sequence 470 AA;

120 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT Gaps 16; Indels 12; 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTG-Length 470; Score 607; DB 5; Pred. No. 7.5e-49; 9; Mismatches 16; 72.5%; 76.3%; Conservative Similarity Sest Local Sim Matches 119; Query Match

셤 ઠે d ò 셤

111 AVYYCAR--TYYYDSSGYYHDAFDIWGQGTMVTVSS 144

121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156

RESULT 5 AAW22841

AAW22841 standard; protein; 146 AA

AAW22841;

12-SEP-1997 (first entry)

Human anti-tumour antigen antibody heavy chain variable region. Human; tumour antigen; cancer; monoclonal; antibody; heavy variable region; medicine; pharmacology; biochemistry; CDR; complementarity determining region.

Homo sapiens.

Location/Qualifiers 1. .19 /label= sig_peptide Key Peptide Peptide Region Region

Region

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The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISABS). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and polynucleotides
or preventing immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGY-----IITS
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR; amplify; human; immunoglobulin; variable; heavy chain; placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - for the
                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                          Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA fragment comprising human immunoglobulin Vh genes production of human immunoglobulin in mammalian hosts.
                                                                             New human immune system associated proteins (HISAP) encoding the HISAP, useful for diagnosing, treating or cell proliferative disorders or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMYYCARADNYFDIVTG-YTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                         65.8%; Score 550.5; DB 4; 70.7%; Pred. No. 7.2e-44; iive 13; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunoglobulin variable heavy chain #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą.
                                                                                                                                                     Claim 1; Col 71-72; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR66296 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-JP000603
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.7%
Matches 111; Conservative
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(first entry)
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Au-Young
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-006791/01.
N-PSDB; AAQ78940.
                               WPI; 2001-030926/04.
                                                 N-PSDB; AAC66531
                                                                                                                                                                                                                                                                                                                                             Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9426895-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
07-AUG-1995
Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR66296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYMHWVRQAPGGGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDT 110
                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a human anti-tumour antigen monoclonal antibody (MAD) heavy chain variable region, useful in medicine, pharmacology and biochemistry. The isotype of a MAD secreted by the human/human hybridoma HT was determined to be mu and kappa. Human MAD was purified, and the antigen recognised by human MAD CLN"-IgM identified by western blotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDWTWRILFMVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTG------
                                                                                                                                                                                                                                                                                           Anticancer human monoclonal antibody variable region sequences - and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          system associated protein; HISAP-13; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AMYYCARADNYFDIVTGY---TSHYFDY----WGRGTLV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 586; DB 2;
Pred. No. 1.8e-47;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated protein HISAP-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection; autoimmune disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corley NC,
                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 10; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36215 standard; protein; 236
/label= CDR_2
118. .139
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.8%;
Matches 118; Conservative 6
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                                                                                                                                      95JP-00278266
                                                                                                                                                                       95JP-00278266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lal P,
                                                                                                                                                                                                                                         WPI; 1997-276726/25.
N-PSDB; AAT75422.
                                                                                                                                                                                                                                                                                                              related DNA and RNA
                                                                                                                                                                                                          (HAGI/) HAGIWARA Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                     JP09100300-A
                                                                                                                                    03-OCT-1995;
                                                                                                                                                                         03-OCT-1995;
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RESULT 6 AAB36215

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                                Protein sequences (AAR66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AA76839-7902) were isolated and cloned from a series of cosmid constructs: Y202; Y103, Y21; Y6,Y24; 3-31; M84, M118 and M131, by PCR amplification using primers AA078917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA mas partially digested with TaqI restriction enzyme. The fragments were separated by gel electrophoresis and 35-45 kb fractions were collected. The fragments were ligated with clar-digested cosmid vector pJ881. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The VH openes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                         1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, immunoglobulin, IGFAM-7, IGFAM; immune disorder; cancer;
infection; inflammation; haematopoiesis; AIDS; allergy.
                                                                                                                                                                                                                                               Query Match 65.7%; Score 550; DB 2; Length 117; Best Local Similarity 83.5%; Pred. No. 3.5e-44; Matches 106; Conservative 4; Mismatches 7; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guegler KJ,
  Disclosure; Page 32-33; 130pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 19
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96295 standard; protein; 148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Ig_domain
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/label= IGFAM-7
34. .117
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98US-0113635P.
99US-0128194P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IGFAM-7 immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                     AMYYCAR 127
                                                                                                                                                                                                                                                                                                                                                                                                                            AVYYCAR 117
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                                                                                                                                                                                                                            Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1998;
07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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The present sequence is the human immunoglobulin superfamily protein IGPAM-7. Its gene was isolated from a CDNA library of bladder tumour lissue. It is expressed in reproductive, gastrointestinal and immune and haematopoietic tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's arteriosclerosis, generalitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                     Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-TRAIL-R antibody related clone 0304 protein SEQ ID NO:29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
65.4%; Score 547.5; DB 3;
Best Local Similarity 68.6%; Pred. No. 7.9e-44;
Matches 107; Conservative 11; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AIYYCARGD-----YGNSLDHWGQGNLVTVSS 137
<u>ن</u>
Yang
                                                                                                                                                                                                                                                                                                  Claim 1; Page 83; 105pp; English
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09-AUG-2001; 2001JP-00243040.
11-OCT-2001; 2001JP-00314489.
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Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-2003 (first entry)
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                                                               WPI; 2000-387796/33
N-PSDB; AAA27387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; TRAIL-R1;
antibody therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 148 AA;
   Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200294880-A1.
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Synthetic.
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Lu DAM,
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The present invention describes antibodies or their functional fragments that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies have cytostatic and apoptotic activities, and can be used in antibody therapy. The antibodies can be applied as remedies and preventives of diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful in the therapy of malignant tumours. Remedies produced with the antibodies are highly safe, and avoid hepatotoxicity. The present sequence represents an anti-TRAIL-R antibody amino acid sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer cells and without exerting an effect on normal cells expressing TRAIL-Rs nor inducing injury to hepatocytes, for use in therapy of malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identífication; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDWTWRILFLVAAATSAHSQVQLVQSGAEMKKPGASVKVSCKTSGYTFTN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human colon cancer antigen protein sequence SEQ ID NO:1050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMYYCARADNYFDIVTGYTSHYFDY-----WGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVYYCARS------YGSGSYYRDYYYGMDVWGQGTTVTVSS 145
                                                                                                                                                                                                                                                                                                                                                                                                               65.1%; Score 544.5; DB 6; 67.3%; Pred. No. 1.5e-43; iive 14; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB53510 standard; protein; 146 AA
                                                                                                                                                                        Claim 54; Page 62; 92pp; Japanese.
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                                 2003-120790/11
Kataoka S;
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 109; Conserv
                                                 N-PSDB; ABZ59698,
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 145 AA;
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Mori E,
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called human colon cancer antigens, given in AABS3234 to AABS4006. The human colon cancer antigens, given in AABS3234 to AABS4006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; cheuroprotective, immunomodulatory, gyaecological, gastrointestinal, valuerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymuclectides, can be used in gene therapy. The colon cancer antigen polymuclectides, creatment and diagnosis of colon disorders, such as colon cancer. The polymuclectides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, wounds, renal disorders, reproductive disorders, immune system cardiovascular disorders, reproductive disorders, immune system cardiovascular disorders. AAC9874 to AAC98772 and AABS4007 represent sequences used in the exemplification of the present invention
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diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma;
lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; human.
                                           Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 AVYYCARXRRWELLGMMWD------FDYWGQGTLVTV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody 4B5 heavy chain variable region.
                                                                                                                                                          to AAC98763 encode the human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.6%; Score 540.5; DB 3;
67.5%; Pred. No. 3.6e-43;
iive 12; Mismatches 15;
                                                                                                                      Claim 11; Page 1631; 2104pp; English.
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108; Conservative
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WPI; 2000-587534/55.
N-PSDB; AAC98267.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 146 AA;
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                                                                                                                                                          AAC97991
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Best Local (
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                                                                                                                                   This polypeptide comprises the heavy chain variable region of the recombinant human monoclonal antibody (MAD) 4B5. 4B5 recognises

C antibodies specific for GD2 antigen antibodies. Antibodies specific for GD2 recognise various cancers including glioblastoma, neuroblastoma, compared and/or metastatic melanoma, breast adenocarcinoma, lung carcinoma, colon adenocarcinoma and denocarcinoma. The invention encompasses 4B5 derivatives with immunologic specificity for antibodies specific for GD2. These contributions and prostate adenocarcinoma. The invention encompasses 4B5 derivatives with immunologic specificity for antibodies specific for GD2. These contributions and regions spanning the 4B5 CDRs. Other derivatives include Fab, F(ab/)2, Fab', scrv and isolated heavy and light chains (see also VDJ junction and regions spanning the 4B5 CDRs. Other derivatives include Fab, F(ab/)2, Fab', scrv and isolated heavy and light chains (see also VDJ junction and regions are also provided, and therapeutic plasmids and vectors, including vaccinia virus vectors, comprising these antibody V regions are also provided, and therapeutic plasmids and vectors including vaccinia virus vectors, comprising these controlled fabs has been shown to minic GD2, and is particularly cuseful in generating a host immune response to cancer. Products of the invention can be used in the detection and treatment of e.g. astrocytoma, colligodendroglinma, peptodyma, medulloblastoma, printing and increases includence and encocarcinoma, squamous cell carcinoma, squamous and adenocarcinoma, squamous and adenocarcinoma, prostatic adenocarcinoma, cholangiocarcinoma, presst tumours such as ductal and lobular adenocarcinoma, presst tumours such as ductal and lobular cut adenocarcinoma, prostatic adenocarcinoma, cuterine and ovarian epithelial carcinoma, prostatic adenocarcinoma, cuterine and ovarian epithelial carcinoma, prostatic adenocarcinoma, cuterine and ovarian epithelial adenocarcinoma, prostatic adenocarcinoma cut adenocarcinoma soft tissue sarcoma and l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRVLFLVAAATSARSQVQLVQSGAEVKKPGASVKVSCKASGYT-----FTS 50
                                 antibody 4B5 polynucleotides and polypeptides - used to develop flucts for the diagnosis and treatment of cancers and for prophylactic rapy to reduce risk of recurrence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.5%; Score 540; DB 2; Length 476; 68.6%; Pred. No. 1.6e-42; ive 14; Mismatches 20; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMYYCAR-ADNYFDIVTGYTSHYF--DYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BLyS binding scFv SEQ ID 1722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP45711 standard; protein; 250 AA.
                                                                                                          Claim 1; Page 79-80; 83pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 476 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111
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                                                                        therapy
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This invention describes novel antibodies that immunospecifically bind to be Lymphocyte Stimulator (BLyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunoadulatory, antitheumatic and antiAnDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant ElyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatodia arthitis, immunodeficiency (CVID) propression and activity such as cancer, immunodeficiency (CVID) and activity such as cancer and activity such as cancer and activity such as cancer and activity such as cancer and activity such as cancer and activity such as cancer and activity such as cancer and activity such as cancer and activity such as cancer and activity and activity and activity and activity and activity and activity and activity and activity an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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17-OCT-2000; 2000US-0240B1EP.
16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-0293499P.
                                                                                                                                                                           15-JUN-2001; 2001WO-US019110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 250 AA;
WO200202641-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1999
                                                                                          10-JAN-2002
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the present of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis, and in bone, cartilage, tenden and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukeemias. AAU39510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YSVHWVRQAPGÇGLEWMGRINPNSGATDYAHKFÇGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----WVRQAPGGGLEWMGWTIASNGKTNYAQKFQGRVTWTDTSTNTAYMELRSLRSDDT 114
                                                                                                                                                                                                                                                                                                Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 MDWTWNILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFINNGLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised anti-Fas antibody heavy chain variable region SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised, anti-Fas antibody; mouse hybridoma; autoimmune disease; diagnosis; CDR; complementarity determining region; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AMYYCAR-ADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 AVYYCAREKDNY-----ATGAWFAYWGQGTLVTVSS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 529.5; DB 4
Pred, No. 2.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 511; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY80290 standard; peptide; 135 AA
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                                 16-APR-2001; 2001WO-US008656.
                                                                             18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.83
Matches 108; Conservative
                                                                                                                                                                                                                                               WPI; 2001-611725/70.
                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressive.
                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 746 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP2000014383-A.
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                                                                                                                                                                                                Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY80290;
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Ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX90020 to AAX90029 encode monoclonal antibodies which react with human connective tissue growth factor (CTGP). AAY24369 to AAX24378 represent these monoclonal antibodies. The antibodies are useful in the diagnosis, prevention and treatment of cell proliferation disorders in which CTGF is, implicated, including fibrosis of lung, Kidney, liver and other tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatod arthritis; rheumatic vascular inflammation; hepatitis; and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 YYMHWVRQAPQQGLEWMGWINPNSSGTHYAQMFQGRVTVTRDTSISTAYMELSRLRSDDT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDWTWRISFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKAFWL------HLSPG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New monoclonal antibody reactive with connective tissue growth factor useful in the treatment of cell proliferation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, vaccination, gene therapy, nutritional supplement;
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
cell proliferation disorder, fibrosis; liver cirrhosis; nephritis; skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer; rheumatic vascular inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Match 63.6%; Score 532; DB 2; Length 149; Local Similarity 68.6%; Pred. No. 2.3e-42; es 107; Conservative 9; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:||||||
AVYYCAR----EGIAAAIYGMDVWGQGTTVTVSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                   Takigawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 177-178; 212pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sakamoto S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted protein #2295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU31804 standard; protein; 746 AA
                                                                                                                                                                                                                                            98WO-JP005697,
                                                                                                                                                                                                                                                                                          97JP-00367699.
                                                                                                                                                                                                                                                                                                                                                             (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                              Tezuka K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-430232/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX90021
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                                                                                               Homo sapiens
                                                                                                                                          W09933878-A1
                                                                                                                                                                                                                                                                                                                    15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                 Tamatani T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2001
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Matches

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RESULT 14 AAU31804

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17;

Length 746; Indels

DB 4;

98JP-00204318. 98JP-00204318

03-JUL-1998; 03-JUL-1998;

18-JAN-2000.

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The present invention describes a recombinant antibody (A) which binds to fas antigen, and controls and induces apoptosis in cells which expressed fas antigen. The complementarity determining regions (CDR) of (A) contain amino acid sequences obtained from a mammal other than human, other regions contain amino acid sequences from human and they partly contain modified amino acids. A) has immunosuppressive activity, (A) is used for treating and/or diagnosing autoimmune diseases. The present sequence represents a specifically claimed heavy chain variable region of (A)
                                                                                                                                                                                                       Novel recombinant antibody used for treating and diagnosing autoimmune diseases - is humanized anti-Fas antibody which controls and induces apoptosis in cells expressing fas antigen.
                                                                                                                         (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                      Claim 13; Page 13; 25pp; Japanese.
                                                                                                                                                                 WPI; 2000-199626/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 135 AA;
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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDISISTAYMELSRLTSDDT 120 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60 Gaps 23; Length 135; 63.1%; Score 528.5; DB 3; Length: 66.9%; Pred. No. 4.4e-42; tive 12; Mismatches 17; Indels Best Local Similarity 66.9% Matches 105; Conservative Query Match ò δ g g

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Sequence 6, Appl
Sequence 18, Appl
Sequence 1050, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 172, Ap
Sequence 1723, Ap
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Sequence 1723, Ap
Sequence 123, Appl
Sequence 123, Appl
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                                                                                                                                                                                                                               1 MDWTWRILFLVAAATGAHSQ........GYTSHYFDYWGRGTLVTVSS 156
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| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB-pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB-pep:*
| cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB-pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-925-299-1050
US-09-925-299-1050
US-09-747-669-3
4 US-10-290-703-3
4 US-10-390-986-8
0 US-09-880-748-1723
4 US-10-390-986-12
US-09-880-748-1640
US-09-880-748-1640
US-09-880-748-1640
US-09-880-748-1640
US-09-509-098-46
US-09-509-098-46
US-10-390-986-12
                                                                                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Match Length
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16 522.5 62.4 432 12 US-10-389-223A-10 Sequence 10, Appli 18 522.5 62.4 480 12 US-10-389-223A-4 Sequence 3, Appli 19 522.5 62.4 614 12 US-10-380-428-3 Sequence 3, Appli 20 522.5 62.4 614 12 US-10-380-428-3 Sequence 2, Appli 22 520.5 62.4 658 12 US-10-380-438-1 Sequence 1, Appli 22 520.5 62.4 658 12 US-10-380-428-3 Sequence 4.763, Appli 22 520.5 62.2 249 10 US-09-26-921.108 Sequence 1635, Appli 22 520.5 62.1 139 10 US-09-269-921.115 Sequence 1635, Appli 22 519.5 62.1 139 10 US-09-269-921.115 Sequence 115, Appli 22 519.5 62.1 139 10 US-09-509-16 Sequence 115, Appli 22 519.5 62.1 139 10 US-09-509-16 Sequence 115, Appli 23 519.5 62.1 139 10 US-09-509-18 Sequence 115, Appli 24 US-10-18-253.115 Sequence 115, Appli 24 US-10-18-253.115 Sequence 115, Appli 25 62.1 139 10 US-09-509-18 Sequence 115, Appli 26 61.9 139 10 US-09-509-921-124 Sequence 124, Appli 26 61.9 139 10 US-09-509-921-124 Sequence 125, Appli 27 10 US-09-509-921-124 Sequence 127, Appli 27 5 61.8 139 10 US-09-509-921-125 Sequence 127, Appli 28 517.5 61.8 139 10 US-09-509-921-125 Sequence 127, Appli 28 517.5 61.8 139 10 US-09-509-921-125 Sequence 127, Appli 29 US-09-509-98-16 Sequence 127, Appli 29 US-09-509-98-16 Sequence 127, Appli 29 US-09-509-98-16 Sequence 127, Appli 29 US-09-509-98-17 Sequence 127, Appli 29 US-09-509-98-17 Sequence 127, Appli 24 US-17.5 61.8 139 10 US-09-509-98-17 Sequence 127, Appli 24 US-17.5 61.8 139 10 US-09-509-98-18 Sequence 127, Appli 24 US-17.5 61.8 139 10 US-09-509-98-18 Sequence 127, Appli 24 US-17.5 61.8 139 10 US-09-509-98-18 Sequence 127, Appli 29 US-09-509-98-18 Sequence 129, Appli 20 US-09-509-98-18 Sequence 129, Appli 20 US-09-509-98-18 Sequence 129, Appli 20 US-09-509-98-11

ALIGNMENTS

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RESULT 1

US-10-044-569B-6

Sequence 6, Application US/10044569B

Sequence 6, Application No. US2030175268A1

GENERAL INFORMATION:

APPLICANT: O. Collen Research Foundation vzw
APPLICANT: Jacquenin, Marc G

APPLICANT: Jacquenin, Marc G

APPLICANT: Saint-Remy, Jean-Maries

TITILE OF INVENTION: Method and pharmaccutical composition for preventing
TITILE OF INVENTION: Method and/or treating systemic inflammatory response syndrome
CURRENT APPLICATION NUMBER: US/10/044,569B

CURRENT APPLICATION NUMBER: US 60/261,405

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: US 60/261,405

MUMBER OF SEG ID NOS: 8

SOFTWARE: PATENTIANG DATE: 2001-01-11

NUMBER OF SEG ID NOS: 8

SOFTWARE: PATENTIANG DATE: 2001-01-11

MUMBER OF SEG ID NOS: 8

SOFTWARE: PATENTIANG COMPLEMENTIANG COMPLEMENTIANG REGION NUMBER OF SEG ID NOS: 8

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SOFTWARE:
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TYPE: PRT
ORGANISM: Homo sapiens
SEQ ID NO 1050
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                       FEATURE:
NAME/KEY: SITE
LOCATION: (123)
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Facent No. US2002012658A1
GENERAL INFORMATION:
APPLICANT: TSUJi, Takashi
APPLICANT: TSUJi, Takashi
TITLE OF INVENTION:
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION OF PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION NUMBER: US 2001-99508
FRIOR APPLICATION NUMBER: UP 2001-99508
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                                                                                1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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Pred. No. 7.8e-52;
9; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.5%;
Best Local Similarity 76.3%;
Matches 119; Conservative 9
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US-09-859-053-28
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NAME/KEY: SITE

1. LOCATION: (123)

2. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-299-1050
) LOCATION: (123) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 146;
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                                                                                                                                     Indels
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                                                                                             Query Match 64.6%; Score 540.5; DB 9; Best Local Similarity 67.5%; Pred. No. 8e-46; Matches 108; Conservative 12; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.6%; Score 540.5; DB Best Local Similarity 67.5%; Pred. No. 8e-46; Matches 108; Conservative 12; Mismatches 1
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PAPPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor TITLE OF INVENTION: and Medicinal Uses Thereof FILE OF INVENTION: and Medicinal Uses Thereof FILE REFERENCE: J1-009PCT CURRENT APPLICATION NUMBER: US/10/390,986
FILE REPERENCE: J0-009PCT CURRENT APPLICATION NUMBER: US/09/582,337
PRIOR APPLICATION NUMBER: US/09/582,337
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: J000-06-23
                                                                                                                                               120
                                                                                                                                                                                      80 INPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
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                                                                                   1 MDWTWRVLFLVAAATSARSQVQLVQSGABVKKPGASVKVSCKASGYT------FTS
                               1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                  61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
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Sequence 1722, Application US/09880748

Publication No. US203005937A1

GENERAL INFORMATION:

APPLICANT: Numben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/216,48

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SEQ ID NO 1722

LENGTH: 250

TAVER: DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-25

NUMBER: OF SEQ ID NOS: 3239

SEQ ID NO 1722
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111 ONWFDPWGRGTLVTVSS 127
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US-09-880-748-1722
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US-10-390-986-8
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Publication No. US20030118593A1

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Dan, Michael D.

APPLICANT: Dan, Michael D.

TITLE OF INVENTION: ANTIGEN BINDING FRAGWENTS, DESIGNATED

TITLE OF INVENTION: AND DETECTION OF CANCERS

FILING DATE: 2002-11-08

PRIOR PELLING DATE: 2009-11-21

PRIOR PELLING DATE: 1998-07-07

PRIOR PLING DATE: 1998-07-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FESSERE FOR WINDOWS VERSION 4.0

SEQ ID NO 3

LENGTHER 476
            GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Dan, Michael D.

APPLICANT: Dan, Michael D.

APPLICANT: Dan, Michael D.

APPLICANT: Saleh, Mansoor

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS

TITLE OF INVENTION: AND DETECTION OF CANCERS

FILE REPERENCE: 186082001001

CURRENT APPLICATION NUMBER: US 09/111,286

PRIOR FILING DATE: 1998-07-07

NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.5%; Score 540; DB 9; Length 476; Best Local Similarity 68.6%; Pred. No. 3.5e-45; Matches 109; Conservative 14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AMYYCAR-ADNYFDIVTGYTSHYF--DYWGRGTLVTVSS 156
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 68.6%
Matches 109; Conservative
US20020122807A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-747-669-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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RESULT 10

US-10-390-986-12

Sequence 12, Application US/10390986

Publication No. US20030166011A1

GENERAL INFORMATION:

TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor

TITLE OF INVENTION: and Medicinal Uses Thereof

TITLE OF INVENTION WHERE: US/10/390,986

CURRENT FILING DATE: 2003-03-17

PRIOR PELICATION NUMBER: US/09/582,337

PRIOR PELICATION NUMBER: US/09/582,337

PRIOR APPLICATION NUMBER: US/09/582,337

PRIOR APPLICATION NUMBER: US/09/582,337

PRIOR APPLICATION NUMBER: US/09/582,337

PRIOR APPLICATION NUMBER: US/09/582,337

PRIOR FILING DATE: 1997-12-25

PRIOR FILING DATE: 1997-12-25

PRIOR FILING DATE: 1998-12-15

NUMBER OF SEQ ID NOS: 27

SOUTHWARE: PatentIn Ver. 2.0
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US-09-80-1640

| Sequence 1640, Application US/09880748
| Publication No. US20030059937A1
| GENERAL INFORMATION:
| APPLICATION Thuben et al. |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| FILE REFREEMENT 2000-06-15
| CURRENT APPLICATION NUMBER: US/09/880,748
| CURRENT FILING DATE: 2001-06-15
| PRIOR APPLICATION NUMBER: 60/210,210
| PRIOR PILING DATE: 2000-10-17
| PRIOR APPLICATION NUMBER: 60/240,816
| PRIOR FILING DATE: 2000-10-17
| PRIOR FILING DATE: 2001-03-16
| PRIOR FILING DATE: 2001-03-16
| PRIOR PRILICATION NUMBER: 60/276,248
| PRIOR PRILICATION NUMBER: 60/277,379
| PRIOR PRILICATION NUMBER: 60/277,379
| PRIOR PRILICATION NUMBER: 60/293,499
| PRIOR FILING DATE: 2001-03-21
| PRIOR PRILICATION NUMBER: 60/293,499
| SOFTWARE: PARENTIN VOT: 2.0
| SEQ ID NOS: 3239
| SEQ ID NOS: 3239
| SEQ ID NOS: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.8%; Score 525.5; DB 14; Length 146; Best Local Similarity 67.3%; Pred. No. 2.5e-44; Matches 105; Conservative 9; Mismatches 25; Indels 17;
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CORGANISM: Homo sapiens
US-09-880-748-1640
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US-10-390-986-12
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LENGTH: 146
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVŢMSRDTSISTAYMELSRLTSDDT 120
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US-09-880-748-1723
i Sequence 1723. Application US/09880748
j Publication No. US20030059937A1
i GENERAL INFORMATION:
i APPLICANT: Ruben et al.
i TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
i CURRENT APPLICATION NUMBER: US/09/880,748
i CURRENT APPLICATION NUMBER: 60/212,210
i PRIOR APPLICATION NUMBER: 60/212,210
i PRIOR FILING DATE: 2000-10-17
i PRIOR APPLICATION NUMBER: 60/240,816
i PRIOR FILING DATE: 2001-06-15
i PRIOR FILING DATE: 2001-03-16
i PRIOR FILING DATE: 2001-03-16
i PRIOR FILING DATE: 2001-03-16
i PRIOR FILING DATE: 2001-03-16
i PRIOR FILING DATE: 2001-03-16
i PRIOR FILING DATE: 2001-03-16
i PRIOR FILING DATE: 2001-03-16
i PRIOR FILING DATE: 2001-03-16
i PRIOR FILING DATE: 2001-03-16
i PRIOR APPLICATION NUMBER: 60/293,499
i RAIOR FILING DATE: 2001-05-25
i NUMBER: OF SEQUENCE: 2001-05-25
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                                                                                                                                                                                                                                                                                                                                  63.6%; Score 532; DB 14; Length 149; 68.6%; Pred. No. 5.7e-45; tive 9; Mismatches 26; Indels 1.
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                                      P1998-356183
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PRIOR APPLICATION NUMBER: JP P19;
PRIOR FILING DATE: 1998-12-15;
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 149
TYPE: PRT
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Best Local Similarity 68.65
Matches 107; Conservative
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US-09-880-748-1723
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US-10-390-986-8
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LENGTH: 250
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OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody H chain V region OTHER INFORMATION: version p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 YWMQWVRQAPGQGLEWMGSIFPGDGDTRYSQKFKGRVTWTADTSTSTAYMELSSLRSEDT 110
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                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Humanized H chain OTHER INFORMATION: region (version p) of anti-HM1.24 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKFGASVKVSCKTSGYNFTGYSASGHIFTA
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 139;
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publication No. US20030129185A1

GENERAL INFORMATION:
APPLICANT: Oncomo, Toshiniko
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yoshinara, Yasushi
APPLICANT: Yoshinara, Yasushi
APPLICANT: Koishinara, Yasushi
APPLICANT: Koishinara, Yasushi
APPLICANT: Koishinara, Yasushi
APPLICANT: Koishinara, Yasushi
APPLICANT: Woshinara, Yasushi
APPLICANT: Woshinara, Yasushi
APPLICANT: Woshinara, Yasushi
APPLICANT: Woshinara, Yasushi
APPLICANT: NOWHER: US/10/218,253
CURRENT FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: US/09/269,921
PRIOR APPLICATION NUMBER: US/09/269,921
PRIOR PILING DATE: 1999-10-03
PRIOR PILING DATE: 1999-10-03
PRIOR FILING DATE: 1996-10-04
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.5%; Score 523.5; DB 1
Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24
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62.5%; Score 523.5; DB 1
Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24
PRIOR APPLICATION NUMBER: JP 9-
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 203
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 46
LENGTH: 139
                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                            51 INPNSGGTNYAQKFQGW/TMTRDTSISTAYMELSSLRSEDTAVYYCARARGSYDIIJGYY 110
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                                                                                                                                                          80 INPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGY- 138
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                                                                                          1 OVOLVOSGAEVKKPGSSVKVSCKASGYTFTG-----YYMHWVRQAPGQGLEWMGW 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NESO1-123
Sequence 123, Application US/09269921
Fublication No. US20030045691A1
GENERAL INFORMATION:
APPLICANT: Onco, Koichiro
APPLICANT: Ohcomo, Toshihiko
APPLICANT: Tochomy, Toshihiko
APPLICANT: Toshihura, Yasushi
APPLICANT: Koishihara, Yasushi
APPLICANT: Normanary APPLICANTON NUMBER: US/09/269,921
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: DOT
BEARLIER FILING DATE: 1997-10-03
EARLIER FILING DATE: 1997-10-04
MUMBER OF SEQ ID NOS: 137
NUMBER OF SEQ ID NOS: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.5%; Score 523.5; DB 10; Length Best Local Similarity 66.7%; Pred. No. 3.7e-44; Matches 104; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 AVYYCARG----LRRG--GYYFDYWGQGTTVTVSS 139
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US-09-509-098-46
Squence 46, Application US/09509098
Squence 46, Application US/09509098
Publication No. US2003103970A1
GENERAL INFORMATION:
APPLICANT: TSUCHTYA, MASAYUKI
TILLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
CURRENT APPLICATION NUMBER: US/09/509,098
CURRENT FILING DATE: 2000-03-22
PRIOR FILING DATE: 1998-10-02
                                                                                                                                                                                                                                                                                   139 --TSHYFDYWGRGTLVTVSS 156
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SEQ ID NO 123
LENGTH: 139
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Best Local Similarity 67.3%; Pred. No. 3.9e-44;
Matches 105; Conservative 9; Mismatches 25; Indels 17; Gaps
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            |:||||| | ||||| AVYYCARG----LRRG--GYYFDYWGQGTTVTVSS 139
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US-10-390-986-10
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Search completed: April 5, 2004, 13:59:14 Job time : 37.6904 secs

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DISKETE
COMPATING SYSTEM: DOS
SOFTWARE: FASISED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER: 336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 336
RICH DATE:
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SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
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TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNONOTO1
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STATE: CP
COUNTRY:
Sequence 8, Appliseduce 12, Appliseduce 28, Appliseduce 10, Appliseduce 112, Appliseduce 11
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Sequence 94, Appl
Sequence 94, Appl
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575.678 Million cell updates/sec
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Sequence 100,
Sequence 100,
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Seguence 102
Seguence 102
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1 MDWTWRILFLVAAATGAHSQ.......GYTSHYFDYWGRGTLVTVSS 156
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2: /cgn2 6/ptodata/2/iaa/5B COMB.pep:*
3: /cgn2 6/ptodata/2/iaa/6A COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/6B COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/pcTus COMB.pep:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-545-809A-90
US-09-582-337-12
US-09-582-337-10
US-09-582-337-10
US-09-582-337-10
US-09-137-117D-112
US-08-137-117D-112
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US-08-137-117D-103
US-08-136-1038-43
US-09-301-393-43
US-09-301-393-43
US-09-455-809A-45
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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APPLICANT: Japan Tobacco, Inc.

TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor TITLE OF INVENTION: and Medicinal Uses Thereof
FILE REPERENCE: J1-009PCT

CURRENT FILING DATE: J000-06-23

PRIOR PILING DATE: J097-12-25

PRIOR FILING DATE: J997-12-25

PRIOR FILING DATE: J998-12-15

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0
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Pred. No. 5.7e-47;
9; Mismatches 26; Indels
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| 12 AVYYCAR-----EGIAAAAIYGMDVWGQGTTVTVSS 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09582337
Patent No. 6562618
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09582337; Patent No. 6562618; GENERAL INFORMATION:
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Best Local Similarity 68.6%;
Matches 107; Conservative
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US-09-582-337-8
                                                                                                                                                                                                               111 AVYYCAR 117
                                                                                                                                 121 AMYYCAR 127
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Best Local Similarity
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PRT
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Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matesuda, Fumiliko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    19;
                                                                                                                                          Length 236;
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                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AMYYCARADNYFDIVTG-YTSHYFDYWGRGTLVTVSS 156
                                                                                                                                      DB 3;
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ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
APPLICATION NUMBER: US/066
REPERENCE/COCKT NUMBER: 29,066
REFERENCE/COCKT NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
                                                                                                                                 65.8%; Score 550.5; DB 3 70.7%; Pred. No. 1.3e-48; iive 13; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston
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INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                 Query Match
Best Local Similarity 70.7%
Matches 111; Conservative
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                     ; CLONE: 3551457
US-09-049-672A-13
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Sequence 10, Application US/09582337

Sequence 10, Application US/09582337

Patent No. 6562618

GENERAL INFORMATION:

APPLICANT: Japan Tobacco, Inc.

TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor

TITLE OF INVENTION: and Medicinal Uses Thereof

FILE REFERENCE: J1-099PCT

CURRENT APPLICATION NUMBER: US/09/582,337

CURRENT FILING DATE: 2000-06-23

FRIOR APPLICATION NUMBER: UP P1997-367699

FRIOR FILING DATE: 1997-12-25

PRIOR FILING DATE: 1988-12-15

SPRIOR FILING DATE: 1988-12-15

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 10

SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 146;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.5%; Score 523.5; DB 4; Best Local Similarity 67.3%; Pred. No. 4.1e-46; Matches 105; Conservative 9; Mismatches 25;
                                                                   121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                               111 AVYYCASRD--YD----YDGRYFDYWGQGTLVTVSS 140
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; Patent No. 5795965
; Gent No. 5795965
; APPLICANT: STOCHIYA, Masayuki
APPLICANT: STOCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TOTTLE OF INVENTION: RESHAPED HUMAN ANTIBODY TOTTLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEV F. T.
STREET.
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
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COUNTRY: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-09-582-337-10
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US-09-582-337-10
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                                                                                                                                      ---LTE 50
                                                                   1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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APPLICANT: Rettleborough, Catherine A.
APPLICANT: Rettleborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS: 42
CORRESPONDENCE ADDRESS: 42
CORRESPONDENCE ADDRESS: 51
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlingen
STATE: Virginia
COUNTY: U.S.A.
ZIP: A2201
CONFUTER: READABLE FORM:
MONOTIVER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Plant PROCOMPATIBLE FORM:
COMPUTER: Plant PROCOMPATIBLE FORM:
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       25; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,421
FILING DATE: US/07/946,421
CLASSIFICATION 0424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 04-MAR-1992
PRIOR APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 06-MAR-1991
ATTONNEY/AGENT INPORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
                                                                                                                                                                                                                                                                                                                                     121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                     111 AVYYCATS-----TVVTPWYFDYWGQGTLVTVSS 139
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       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/07946421
Patent No. 5558864
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 140 aming
       105; Conservative
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       Matches
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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDŢSISTAYMELSRLTSDDŢ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: KIYOSHI, Kazuhiko
APPLICANT: HIGUCHI, Hirofumi
APPLICANT: TOKTYOSHI, Sachio
ITIZE OF INVENTION: SANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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419 Seventh Street, N.W., Suite 300
                                                                              FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
FILING DATE: 24-APR-1992
FILING DATE: 39-APR-1992
FILING DATE: 19-FEB-1992
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HALOH G.
RESTRATION NUMBER: 53-466/126/AAOK
TELECOMONIOLATION INFORMATION:
TELECOMONIOLATION INFORMATION:
TELECOMONIOLATION INFORMATION:
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TELECOMONIOLATION INFORMATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.2%; Score 520.5;
65.4%; Pred. No. 7.6e
:ive 13; Mismatches
                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
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Patent No. 6114143

    Floppy disk
    IBM PC compati

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amino acid
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02; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acir
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Simi
Matches 102;
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US-08-513-968-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 135;
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Patent No. 5817790

GENERAL INFORMATION

APPLICANT: SATO, Koh

APPLICANT: SATO, Koh

APPLICANT: SATO, Koh

APPLICANT: SALDANHA, Jose

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLGY & Lardner

STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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20;
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APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
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Pred. No. 7.6e-
13, Mismatches
                                              CLASSIFICATION 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA;
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
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Best Local Similarity 65.4
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-137-117D-112
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STATE: D.C.
COUNTRY: USA
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TOPOLOGY: linear
MOLECULE TYPE: polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6 Becker Fa
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
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                                                                                                                                                                                                                                RESULT 11
US-08-477-877B-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 YTWHWVRQAPGQGLEWIGGINPNNGDISYTQKFKGKATMTVDTSTNTAYMELSSLRSEDT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDWTWRVFFLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYT-----FTP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of H chain V region version r of OTHER INFORMATION: humanized anti-HMI.24 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KOSIBIHARA, YASUO
APPLICANT: XOSIBIHARA, YASUO
APPLICANT: XOSIBIHARA, YASUSHI
ITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REPERRORS:
CURRENT APPLICATION NUMBER: US/09/355,925
CURRENT FILING DATE: 1999-08-11
FRIOR APPLICATION NUMBER: DF 910 PRIOR FILING DATE: 1998-02-12
FRIOR APPLICATION NUMBER: DF 941410
FRIOR APPLICATION NUMBER: JP 941410
FRIOR FILING DATE: 1997-02-12
FRIOR FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTING VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 AVYYCA------rPYYAYAIDSWGQGTLVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.8%; Score 517.5; DB 4; Best Local Similarity 66.0%; Pred. No. 1.6e-45; Matches 103; Conservative 11; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 517.5; DB 3; Pred. No. 1.6e-45; 15; Mismatches 22
APPLICATION NUMBER: US/08/513,968
FILING DATE: 11.5EP-1995
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 78913/1993
FILING DATE: 11.MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER I.
REGISTRATION NUMBER: 25,618
REJERPANENCE/DOCKET NUMBER: EDA=1
TELEPHONE: 202-628-5197
TELEFEX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09355925
Patent No. 6503510
                                                                                                                                                                                                                                                                                             TELEX: 248633
INFORMATION FOR SEQ. ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.1%;
Matches 100; Conservative 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-513-968-38
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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80 INPNSGATDYAHKFOGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
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61.6%; Score 516; DB 2; Length 123;
Best Local Similarity 74.5%; Pred. No. 2e-45;
Matches 102; Conservative 8; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS: 86
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Human Amu 5-3 heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DUS
SOFTWARE:
Worderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,963B
FILING DATE: 07-424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-WAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 05-WAR-1993
APPLICATION NUMBER: 08/1027,008
FILING DATE: 05-WAR-1993
ATOMARE: OS-WAR-1993

                                                  Sequence 94, Application US/08477989B
Patent No. 5951983
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 3.5 inch diskette COMPUTER: IBM PS/2 ODERATING SYSTEM: MS-DOS ACHTURANTE
                                                                                                                                                                                                                                                                    Kieber-Emmons, Thomas
                                                                                                                                                                                                                                                                                                 Postema, Christina E.
White-Scharf, Mary
                                                                                                                                                    Bazin, Herv
Latinne, Dominique
Kaplan, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 SHYFDYWGRGTLVTVSS 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIF: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Jersey
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6 Becker CITY: Roseland STAIE: New Jers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
US-08-477-989B-94
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                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                        RESULT 12
US-08-472-281A-94
US-08-472-281A-94
Sequence 94, Application US/08472281A
Fatent No. 5817311
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Brine, Bain, Gilfillan,
ADDRESSEE: Carella, Stewart & Olstein
ADDRESSEE: Carella, Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 INPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 INPNSGGINYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGRTEYIVV---- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTG------YYMHWVRQAPGQGLEWMGR 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 61.6%; Score 516; DB 2; Length 123; Best Local Similarity 74.5%; Pred. No. 2e-45; Matches 102; Conservative 8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: Human Amu 5-3 heavy chain variable region.
US-08-472-281A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Secount, Scewart & OISTEIN STREET: New Jersey
CUUNTRY: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: NS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILING DATE: 29-MAR-1995
FILING DATE: 29-MAR-1995
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Olstein, Elliot M. REGISTRATION NUMBER: 24,025 REFERENCE/DOCKET NUMBER: 61,1 FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 SHYFDYWGRGTLVTVSS 156
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140 SHYFDYWGRGTLVTVSS 156
                                               107 AEGFDYWGQGTLVTVSS 123
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MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 123 amin TYPP
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TYPE: amino acid
STRANDEDNESS:
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107 AEGFDYWGQGTLVTVSS 123

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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.5%; Score 514.5; DB 2; Length 135; 64.1%; Pred. No. 3.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                        APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: SALONIS, Steven
APPLICANT: SALONINA, Jose
APPLICANT: SALONINA, NESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPEDIBENCE ADDRESS:
ADDRESSEE: FOLSY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE: CASSIFICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US/08/137,117
APPLICATION NUMBER: US/08/137,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---RFAYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.1e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 4-32084
FILING DATE: JP-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAYOLD C.
                  Sequence 102, Application US/08436717; Patent No. 5817790; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
STATE: D.C.
COUNTY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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REFERENCE/DOCKET NUMBER: 534
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                            3: Foley & Lardner 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 135 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 AVYYCARGGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 64.1
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-436-717-102
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US-08-436-717-102
                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDWIWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYS-----FTS
                          US-08-137-117D-102

Sequence 102 Application US/08137117D

Sequence 102 Application US/08137117D

Sequence 102 Application US/08137117D

SEQUENCAL INFORMATION:

APPLICANT: STATC, Koh

APPLICANT: BENDIG, Mary

APPLICANT: SALDANA, Jose

TITLE OF INVENTION: INFERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROLGY & Larder

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STRET: DC.

COMPUTER: BENDIG Street

MEDLIM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PLOSG/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 43.2084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION NUMBER: US 43.2084

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 43.2084

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 43.2084

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 5.258

REGISTRATION INDEMATION:

NAME: WEGNER, Harold C.

REGISTRATION INDEMATION:

NAME: WEGNER, Harold C.

REGISTRATION INDEMATION:

REGISTRATION INDEMATION:

NAME: WEGNER, Harold C.

REGISTRATION INDEMATION:

TELECOMMUNICATION INDEMATION:
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Best Local Similarity 64.19
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-137-117D-102
                     RESULT 14
US-08-137-117D-102
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Search completed: April 5, 2004, 13:44:09 Job time : 14.9898 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

April Run on:

5, 2004, 13:25:01; Search time 11.6142 Seconds (without alignments) 1184.358 Million cell updates/sec

Perfect score:

US-10-044-569B-8 738 1 METPAÇLLFLLLWLPDTTG.....TKVEIKRTVAAPSVFIFPPS 143 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AL IGNMENTS

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Ig Kappa chain - human

1g Kappa chain - human

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens

C.Species: Howo sapiens

C.Accession: S20631

R.Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.

R.Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.

A.Reference number: S20631

A.Reference number: S20631

A.Scession: S20631

A.Scession: S20631

A.Stesidues: 1-145 - LEB-

A.Residues: 1-145 - LEB-

A.Crose-references: RMRA

A.Residues: 1-145 - LEB-

A.Crose-references: RMRL: S11903; NID: g331156; PIDN: CAA77955.1; PID: g331157

C.Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F; 36-111/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGQAPRLLIYGASSRATDIPHRESGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PGQAPSLVIYGVSIRATGIPDRFSGSGSETDFTLTISRLEFEDFAVYCHQYGYTP-LTF 119
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84.8%; Score 625.5; DB 2;
Best Local Similarity 86.0%; Pred. No. 1.3e-44;
Matches 123; Conservative 5; Mismatches 14;
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RESULT 2 PL0106

Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PLO106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
A;Tille: Relationship of variable region genes expressed by a human B cell lymphoma sec
A;Reference number: PLO106; MUID:89235583; PMID:2541221
A;Accession: PLO106.

A;Molecule type: mRNA
A;Residues: 1-144 <SIL>
C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
E;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Domain: V region <VRE>

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A;Gener: GDB:IGKV3
A;Gross-references: GDB:136266
A;Gross-references: GDB:136266
A;Gross-references: GDB:136266
A;Gross-references: GDB:136266
A;Gross-references: GDB:136266
A;Gross-references: GDB:136266
A;Gross-references: GDB:136266
A;Gross-reference: GDB:IGHT B;Gross-reference and GDB:IGHT B;Gross-reference and GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-reference: GDB:IGHT B;Gross-refe
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                                                                                                                                                                                                                                            expressed
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                                                                                     C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METPAQLIFLILIMIPDITGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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                                                                                                                                        C,Accession: PL0021
R,Kipps, T.J.; Tomhave, B.; Chen, P.P.; Carson, D.A.
D. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene A;Reference number: PL0021; MUID:88171307; PMID:3127527
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Pred. No. 2.8e-42;
4; Mismatches 7;
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Pred. No. 1.9e-42;
3; Mismatches 7;
                                                      - human
                                                   Ig kappa chain precursor V-III region (Hic)
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90.8%;
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ilarity 91.5%;
Conservative 3
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C,Comment: The protein is one of
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Best Local Similarity 90.8
Matches 118; Conservative
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Best Local Similarity
Matches 119; Conserv
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A;Residues: 1-129 <MAH>
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A/Map position: 2p12-pp1

C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region, immunoglobulin homology charactionatically, chronic lymphocytic leukemia, heterotetramer; immunoglobulin F;11-20/Domain: signal sequence #status predicted <SIG>F;21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>F;21-11/Pomain: immunoglobulin homology <IMM>F;21-11/Domain: immunoglobulin homology <IMM>F;71-17/Region: complementarity-determining 2
F;110-17/Region: complementarity-determining 3
F;110-17/Region: complementarity-determining 3
F;118-129/Region: J segment (JKI)
F;31-129/Region: J segment (JKI)
F;31-129/Region: J segment (JKI)
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C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Exp. Med. 167, 840-852, 1988
A.Fittle: Autoantibody-associated kappa light chain variable region gene expressed in
A.Reference number: PL0021; MUID:88171307; PMID:3127527
A.Recession: PL0022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF
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Pred. No. 2.9e-43;
2; Mismatches 6;
                                                                                                                                                                                                         Query Match
83.9%; Score 619; DB
Best Local Similarity 88.1%; Pred. No. 4.4e-
Matches 126; Conservative 5; Mismatches
                    F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-115/Region: complementarity-determining 3
F;108-127/Domain: J region (RG)
F;128-144/Domain: C region (fragment) <CRE>
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immunoglobulin homology
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93.1%;
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Best Local Similarity 93.1
Matches 121; Conservative
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A; Residues: 1-129 < KIP>
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Ig kappa chain V region - human (fragment)
CjSpecies: Homo sapiens (man)
CjSpecies: Homo sapiens (man)
CjDate: O6-Jan.1995 #sequence_revision 06-Jan.1995 #text_change 21-Jan-2000
CjAccession: 638643 #sequence_revision No. Janstagner, P.; Zouali, M. RjBensimon, C.; Chastagner, P.; Zouali, M. Submitted to the EMBL Data Library, November 1993
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
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PGQAPRILLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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Cibace: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Cibacession: 340325
Rixlein, R.; Jaenichen, R.; Zachau, H.G.
Rixlein, R.; Jaenichen, R.; Zachau, H.G.
A.;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
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                                          61 PGQAPKLLIYGASSRATGIPDRFSGSGSGTDFTLTISKLEPEDFAVYXCQQYGSSP-FPF
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Pred. No. 2.3e-41;
6; Mismatches 8;
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A,Scatus: preliminary: translation not shown
A,Molecule type: mRNA
A,Residues: 1-129 <KLE>
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Best Local Similarity 88.5%;
Matches 115; Conservative
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Gogtreeikk 129
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Best Local Similarity
Matches 109; Conserv
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A;Molecule type: mRNA
A;Residues: 1-134 <BEN>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C; Accession: S4636; 1994
A; The ference number: S46369; MUID: 94313975; PMID: 8039491
A; Reference number: S46369; MUID: 94313975; PMID: 8039491
A; Reference number: S46369
A; Residues: 1129 < REN>
A; Residues: 1129 < REN>
A; Csuperfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: immunoglobulin homology < INUM>
F; 36-111/Domain: immunoglobulin homology < NUM>
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S4.Reference number: S20636
S5.Reference number: S2
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                                                                      PGOAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                  61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP-QTF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
       METPAQLLFLLLMLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK 60
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88.5%; Pred. No. 2.3e-41;
iive 6; Mismatches 8;
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                                                                                                                                                                                                     GGGTKVEIKR 130
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Best Local Similarity
Matches 115; Conserv
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62 GQAPRLLIYGASSRATDIPHRFSGGSGTDFTL/ISRLEPEDFAVYYCQQYGTSALLTFG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $40360
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40360
A;Reference number: $40360
                                                                                                                                                                                                                                                                                              | Species: Homo sapiens (man)
| Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                              61 PGQAPRLLIYGVSSRATGIPDRFSGSASGTDFTLTISRLEPEDFAVYCQHYGGSPRBYT
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                      PGQAPRILLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSAL-LT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X72456; NID:g441380; PIDN:CAA51124.1; PID:g441381 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;35-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-200
C;Accession: $40346
C;Accession: $40346
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40346
A;Status: preliminary; translation not shown
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Pred. No. 8.3e-40;
4; Mismatches 12;
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Pred. No. 5.2e-40;
9; Mismatches 12;
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86.9%;
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ilarity 84.0%;
Conservative
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Best Local Similarity 86.9
Matches 113; Conservative
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                                                                                                                FGGGTKVEIK
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Best Local Simil
Matches 110; (
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R; Newkirk, M.M.; Gram, H.; Heinrich, G.F.; Oestberg, L.; Capra, J.D.; Wasserman, R.L.
J. Clin. Invest. 81, 1511-1518, 1988
A; Title: Complete protein sequences of the variable regions of the cloned heavy and ligh actors of the Wa idiotypic family.
A; Reference number: A92767; MUID:88213701; PMID:2452836
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A.Residues: 1-130 **CLEE> .
A.Cross-references: EMBL:211890; NID:g33202; FIDN:CAA77944.1; PID:g33203; EMBL:211895;
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotecramer; immunoglobulin homology <IMM>
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60
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A.Residues: 1-129 <NEW>
A.Residues: 1-129 <NEW>
A.Residues: 1-129 <NEW>
A.Cross-references: GB:M20031
A.Note: the authors translated the codon GAT for residue 17 as Ala
A.Note: this sequence was determined from the differentiated gene
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamils: sequence #status predicted <SIG>
F.21-129/Product: Ig kappa chain V-III region EVI-15 #status predicted <KV3>
F.36-111/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Dacession: S20637; Becquence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20637; S20632
R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
                                                                                                                                                                                                                                                  Species: Homo sapiens (man)
Date: 31-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
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Pred. No. 2.6e-40;
2; Mismatches 11;
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Pred. No. 3.9e-40;
2; Mismatches 13;
                                                                                                                                                                                                                                 kappa chain precursor V-III region (EVI-15)
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ilarity 87.7%;
Conservative
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Best Local Similarity 89.2
Matches 116; Conservative
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A, Accession: S20637
A, Status: preliminary
A, Molecule type: mRNA
                                                                                                                PGTKVDIRR
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61 APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDPAVFYCQOYGSSP-ITFGGG 119
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A, Status: not compared with conceptual translation
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A, Status: not compared with conceptual translation
A, Molecule type: DNA
A, Note: this sequence was translated from an aberrantly rearranged kappa gene from lambd
A, Note: this sequence was translated from an aberrantly rearranged kappa gene from lambd
A, Note: this sequence was translated from an aberrantly rearranged kappa gene from lambd
A, Note: this sequence was translated from an aberrantly rearranged kappa gene from lambd
C, Sequentian: 27
A, Introns: 17/1
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin pomology cIMM>
F, 111/Domain: immunoglobulin homology cIMM>
                                                                                                                                                                                                                                                                                                                                               Ig Kappa chain precursor V-III (Nalm-6) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 19.Nov-1988 #sequence_revision 19.Nov-1988 #text_change 21-Jan-2000 C;Accession: B27594 RsGraninger, W.B.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J.; Korsmeyer, S.J. B;Graninger, W.B.; Geleting element. Germline and rearranged, duplicated and dispersed A;Teile: The kappa-deleting element. Germline and rearranged, duplicated and dispersed A;Reference number: A92779; MUID:88154739; PMID:3126251
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             PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                 61 PGQAPRLLIYDASNRATGIPDRFSGSGSGTDFTLTISRLEPQDFAVYYCQHYGRSPPLTF 120
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C.Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C.Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C.Accession: S40327
B.Y. Januarol. 23, 3348-3271, 1993
A.Title: Expressed human immunoglobulin chi genes and their hypermutation. A.Reference number: S40312; MUID:94080991; PMID:8258341
A.Accession: S40327
A.Status: preliminary; translation not shown
A.Molecule type: mRNA
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A;Coss-references: EMBL:X72437; NID:G441342; PIDN:CAA51105.1; PID:g441343
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-108/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.4e-39;
6; Mismatches 5;
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illarity 90.2%;
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PO1601 P P04430 P P01610 P P01610 P P01604 P P06309 P P01664 m P01666 m P01666 m P01663 P P01663 P

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PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=88171307; PubMed=3127527;
Kipps T.J., Tonhave E., Chen P.P., Carson D.A.;
Kipps T.J., Tonhave E., Chen P.P., Carson D.A.;
Mutcantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-!- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                             Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG KAPPA CHAIN V-III REGION HAH.
FRAMEWORK-1.
COMPLEMBIYARITY-DETERMINING-1.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMBIYARITY-DETERMINING-3.
JKI SEGNENT.
BY SIMILARITY.
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                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
119 Kappa chain V-III region HAH precursor.
Homo sapiens (Human)
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PIR; PL0022; KJHUHA.
HSSP; P80362; INTL.
GO; GO:000557; C:extracellular; NAS.
GO; GO:000557; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig-v.
Pfam; PF00047; ig; 1.
SWART; SW00406; IGv; 1.
PROAITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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                         KV1F HUMAN
KV1E HUMAN
KV1L HUMAN
KV3L HUMAN
KV3L MUUSE
KV3L MUUSE
KV3N MOUSE
KV3U HUMAN
KV3T MOUSE
       STANDARD;
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       RESULT 1
KV3L HUMAN
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1139.758 Million cell updates/sec
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738
1 METPAQLLFLLLLMLPDTTG......TKVEIKRTVAAPSVFIFPPS
                                                                    April 5, 2004, 12:10:21; Search time 6.533 Seconds
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                      141681 seqs, 52070155 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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d à d RESULT 2 KV3M_HUMAN

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRAMENOKR-1.
COMPLEMENNARITY-DETERMINING-1.
FRAMEWORK-2.
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MEDLINE-86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Hunan immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCEL TaxID=9606;
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Pred. No. 9e-45;
3; Mismatches 14; Indels
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JKI SEGMENTY.
BY SIMILARITY.
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                                                                   P063II,
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G Kappa chain V-III region IARC/BL41 precursor.
Homo sapiens (Human).
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                                     128 AA
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PIR; A01899; KRHU41.
HSSP; P01607; IREI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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85.4%;
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                                     STANDARD;
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SMART, SM00406, IGV
PROSITE, PS50835, I
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P04207;
                                     HUMAN
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PGQAPRILIYGASSRATGIPDRFSGSGSGTDFTLITSRLEPEDFAVYYCQQYGTSP-RTF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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SEQUENCE FROM N.A.
MEDLINE-88171307; PubMed=3127527;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Mutoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
J. Exp. Med. 167:840-852(1988).
J. Exp. Med. 167:840-852(1988).
J. Exp. Med. 167:840-852(1988).
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J. Exp. Med. 167:840-852(1988).
J. Exp. Med. 167:840-852(1
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ţ,
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Pred. No. 6.9e-51;
3; Mismatches 7; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                             10.1-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
15-UTL-1999 (Rel. 38, Last annotation update)
Homo sapiens (Human).
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HSSP; PR0362; 1MTL.
GO, GO:0005576; Cextracellular; NAS.
GO, GO:0003823; F:antigen binding; NAS.
GO, GO:0006855; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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Immunoglobulin V region; Signal.
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ilarity 91.5%;
Conservative
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                                                                                                            GGGTKVEIKR 130
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129 AA;
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PROSITE; PS50835
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Matches 119;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 METPAQLIFILLIMULPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEAPAÇLLFLLLKWLPDTTGETVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=85087932; PubMed=6440122;
Pech M., Zachau H.G.;
"Immunoglobulingenes of different subgroups are interdigitated within the VK locus",
Nucleic Acids Res. 12:9229-9236(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.6%; Score 506.5; DB 1; Length 115; 91.0%; Pred. No. 4.4e-42; rive 2; Mismatches 7; Indels 1
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PRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-AUG-1999 (Hall region VH precursor (Fragment).
Homo sapiens (Human).
chain V-III region VG precursor (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P80362; IWTL.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding; NAS.

OG; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X01668; -; NOT ANNOTATED CDS. PIR; A01900; K3HUVG.
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MEDLINE=85087932; PubMed=6440122;
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PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .larity 91.0%;
Conservative
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                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 101, Conserv
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                                                                                       NCBI_TaxID=9606;
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SMART; SM0040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KV3J HUMAN
P04434;
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HUMAN
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    SOURCE THE TENT TO BE A PROPERTY OF THE TENT TO BE A PROPERTY OF THE TENT THE TENT TO BE A PROPERTY OF THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                             MEDIINE=86177570; PubMed=3083417; Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P., Jirik F.R., Sarson D.A.; Coldition R., Carson D.A.; "Cloning and sequence determination of a human rheumatoid factor light-chain gene."; Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
20-MAR-1997 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuery Match 72.0%; Score 531.5; DB 1; Length 129; Best Local Similarity 82.3%; Pred. No. 2e-44; Matches 107; Conservative 6; Mismatches 16; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG KAPPA CHAIN V-III REGION CLL. FRANEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRANEWORK-2. COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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-hog 16; Indels
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Last annotation update)
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF004047; 1g; 1.
PROSTIE; PS50835; IG_IKE; 1.
Immunoglobulin V region; Signal.
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GOGTRVEIKR 129
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129
129 AA;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=9606;
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13-AUG-1987
15-JUL-1999
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ID KV3I HUMAN
AC P04433;
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SEQUENCE
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us-10-044-569b-8.rsp

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21 EIVLIGEPGILSLSPGERATLSCRASQSVASAYLAWYQQKPGQAPRLLIYGASSRATDIP 80
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-!- MISCELLANGEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
PIR; A01896; K3HUWL.
HSSP; 880362; MTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
InterPro; IPR007110; Ig-like.
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NCBI_TaxID=9606;
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Pred. No. 1.8e-40;
1; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 109;
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109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.3%; Score 489.5; DB 1;
ilarity 88.2%; Pred. No. 1.8e-40;
Conservative 6; Mismatches 6;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-III region WOL.
Homo sapiens (Human).
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                GO; GO: 0005576; C: extracellular; NAS. GO; GO: 0003823; F: antigen binding; NAS. GO; GO: 0006955; P: immune response; NAS. InterPro; IPR007110; IQ-like.
InterPro; IPR007110; IQ-like.
Pfam; PF00047; iq; IQ-v.
PROSITE; SM0406; IGv; I.
IMMUNGQIOBULIN V FGGION.
DISULEID
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Pfam; PF00047; ig; 1.
SMART; SM0046; igv; 1.
Immunoglobulin V region.
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1 Similarity 90.0%;
99, Conservative
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les 97; Conserv
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                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biochemistry 20:5816-5822(1981).
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA-GLOBULIN ACTIVITY.
PIR; A01892; K3HUSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLIFILLLWIPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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    Pech M., Zachau H.G., "Imminoglobulin genes of different subgroups are interdigitated within the VK locus.", Within the Acids Res. 12:9229-9236(1984).
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Pred. No. 9.7e-42;
5; Mismatches 9; Indels
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COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
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21-JUJ.-1986 (Rel. 01, Last sequence update)
15-JUJ.-1999 (Rel. 38, Last annotation update)
15-JUJ.-1999 (Rel. 38, Last annotation update)
Homo sapiens (Human)
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR005596; Ig_v.
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PIR; A01901; K3HUVH.
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Pfam: PP00047; ig; 1.
SMARK; SM04066; IGv.1.
PROSITE: PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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Surer L., Barnikol H.U., Watanabe S., Hilschmann N.;

MEDLINE=72188439; PubMed=5027703;

Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

Inter L., Barnikol H.U., Watanabe S., Hilschmann N.;

Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

Interpolation L-chain of kappar-type, Bubgroup 3 Bence-Jones protein

Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";

Hoppe-Seyler's Z., Physiol. Chem. 353:189-208(1972).

INTSCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

INTSCELLANEOUS: THIS is a Bence-Jones protein.

MSSP; P80362; IWTL.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0005956; Cextracellular; NAS.

GO; GO:0005956; P:immune response; NAS.

RO; GO:0005969; IRR00110; IG-11ke.

REAPRO; IRR007110; IG-11ke.

REART; SM00406; IG-V.

REART; SM00406; IG-V.

REART; PS00815; IG-IIKE; I.

REART; PS00815; IIRR0174.
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20-MAR-1987 (Rel. 04, Last sequence update)
15-UUL-1998 (Rel. 38, Last annotation update)
15 Suppa chain V-III region GOL (Rheumatoid factor).
19 Kappa chain V-III region GOL (Rheumatoid factor).
19 Kappa chain (Human).
10 Fukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
10 Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
16 kappa chain V-III region Ti.
17-JUL-1999 (Menan).
18 kappa chain (Y-III region Ti.
18 kappa chain (Y-III region Ti.
19 kappota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
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DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG-SLGRTFGQGTKVEIKR 109
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A The basic sequences of immunoglobulin kappa chains: sequence studies for the basic sequence of immunoglobulin kappa chains: sequence studies are of Bance Onnes protein.

B Let L. 2:301-304(1969) .

C -! - MISCELLANEOUS: This is a Bence-Jones protein.

B RISP, P80362; IMTL.

DR PRAN; PR007110; Ig-like.

DR InterPro; IPR003596; Ig.v.

DR PRAN; SM00406; Ig.v.

DR PRAN; SM00406; Ig.v.

DR PROSITE; P850835; IG_LIKE; 1.

DR PROSITE; P850835; IG_LIKE; 1.

DR PRAN; SM00406; IG.v.

DR PROSITE; P850835; IG_LIKE; 1.

DR PROSITE; P850835; IG_LIKE; 1.

DR PROSITE; P850835; IG_LIKE; 1.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                       81 HRFSGSGSGTDFTLTISRLBPEDFAVYYCQQYGTSALLTFGGGTKVEIKR 130
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                                                                                                                                                                                                                                                                         Score 464.5; DB 1; Length 109;
Pred. No. 4.7e-38;
5; Mismatches 11; Indels 1;
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-III region B6.
Homo sapiens (Human).
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HSSP, F80362; INTI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
Ffam; PF0047; ig; 1.
SMART; SM00406; IGV; 1.
FROAIT; PS0047; ig; 1.
FROAIT; PS08035; IG Like; 1.
Imminoglobulin V region.
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84.5%;
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MEDLINE=84093600; PubMed=6419127;

A Bentley D.L.;

Most kappa immunoglobulin mRNA in human lymphocytes is homologous to

I asmall family of germ-line V genes.";

In Nature 307:77-80 (1984).

I. Nature 307:77-80 (1984).

I. Nature 307:77-80 (1984).

I. Nature 307:77-80 (1984).

II.  Nature 307:77-
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"The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IgM anti-gamma globulins.";
Ann. Immunol. (Paris) 127C:261-271(1976).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17 kappa chain V-III region POM.
18 kappa chain V-III region POM.
19 kappa chain (Human).
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                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-III region NG9 precursor (Fragment).
Homo sapiens (Human).
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MEDLINE=76276460; PubMed=60899;
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Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
Zachau H.G.;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 HRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ARFSGSGSGTEFTLTISSLQSEDFAVYXCQQYNNWP-PTFGQGTRVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                      109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.2%; Score 422.5; DB 1; 76.4%; Pred. No. 5.2e-34; iive 11; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-IV region JI precursor.
Homo sapiens (Human)
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PIR; A01897; K3HUPM.
HSSP, P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR03596; Ig-v.
Pfam; PR00406; Ig, v.
Pfam; PR00406; Ig, v.
PRART; SM0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V regin.
DISULPID
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Nucleic Acids Res. 13:6515-6529(1985).
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SWART; SM00406; iGv, i.
SMO0406; iGv, i.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                            56 WYQQKPGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS 115
                                                                                                                                                                                         1 METPAQLLFLLLLMLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASA----YLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-85014148; PubMed=6091049;
Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                   56.6%; Score 417.5; DB 1; Length 133; larity 62.2%; Pred. No. 2e-33; Conservative 18; Mismatches 26; Indels 7;
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                    COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                             133
14632 MW; 5FB3953066744AF4 CRC64;
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13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
16 Kappa chain V-I region Walker precursor.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                           129 AA
                                                                 SIMILARITY
                          FRAMEWORK-3
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:000855; F:immune response; NAS.
InterPro; IPR00710; IG-like.
InterPro; IPR003596; Ig_v.
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                                                                                                     Query Match
Best Local Similarity
61
76
83
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123
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133 AA;
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62 PGKAPKLLIYAASSLQSGVTSRFSGSGSGTDFTLTISSLQPEDSATYYCQQ-SYSTLITF 120
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                                                                                                                                                3 MRVPAQLIGILILMIRGARCDIQMIQSPSSLSASAVGDRVTITCRASQSI-SNYLNWYQQK
                                                                                                                                  1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                       Gaps
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                                                                           54.7%; Score 404; DB 1; Length 129; 64.3%; Pred. No. 3.8e-32; ive 15; Mismatches 29; Indels
COMPLEMENTARITY - DETERMINING - 3
                                                     14069 MW; F941FA07D4AFC2F9 CRC64;
              FRAMEWORK-4.
BY SIMILARITY
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83; Conservative
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121 GQGTRLEIK 129
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECURINCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UL78;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin Immunol, Immunopathol. 87:184-192(1998).
EMBL, AF035036, AAD56272.1; -.
PIR, A30601, A30601.
PIR, B30601, B30601.
PIR, B30601, B30607.
PIR, B30607, B30607.
PIR, C30601, C30607.
PIR, C30601, C30607.
PIR, C30608, C30608.
PIR, D30607, D30607.
PIR, D30608, D30608.
PIR, D30608, D30608.
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Q811C3
Q91WF8
Q91WS9
Q91WS9
Q8K1F1
Q7TWK0
Q9UL70
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Q9RN12
Q9RX1F3
Q9RX1F3
Q9CXF0
Q9QYF0
Q8VIJO
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07TQM2
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Q920E6
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Homo sapiens (Human)
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F30608.
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08tcd0 homo sapien
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Copyright (c) 1993 - 2004 Compugen Ltd.
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109 AA.

ALIGNMENTS

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Hypothetical protein.
Homo sapiens (Human).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                Length 109;
                                                                                                                                                                                                                                                                             MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
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Pred, No. 1.1e-41;
5; Mismatches 8;
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Best Local Similarity 91.8%; Pred. No. 6.3e-44;
Matches 101; Conservative 3; Mismatches 5;
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Clin. Immunol. Immunopathol. 87:184-192(1998)
BMB1, AF035028; AADS6264.1; -.
PIR; B30607; B30607.
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01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last seg
                                                                                                                                                                                                                                                                                                                                                   PRT;
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InterPro: IPR00390; Ig-like.
InterPro: IPR00390; Ig_v.
Pfam; PF00047; 1g; 1.
SWART; SW00406; IGv; 1.
PIR, PH0963, PH0963.
PIR, SA34096, PH0965.
PIR, SA34096, SA34096.
HSSP, PB0362, 1WTL.
INTERPLO, IPR007110, IG-like.
INTERPLO, IRR03596, IG-V.
Fam, PR0047; ig; I.
SNAAT; SNO0406, IGY; I.
                                                                                                                                    11646 MW;
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                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment).
Homo sapiens (Human)
                                                                                                                                       109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                              NON TER
NON TER
SEQUENCE
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RADIUM=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Duetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raba S.S., McWan P.J., McKernan R.J., Malek J.A., Gunatane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Richards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,

R Rabesley R.M., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Kzzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

R Generation and initial analysis of more than 15,000 full-length human
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                   Eukaryoca, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lung;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0562256; AAH56256.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences.";
l. Acad. Sci. U.S.A. 99:16899-16903(2002)
234 AA
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PRT;
                                                             01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
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PRELIMINARY;
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                       Sest Local Similarity 65.7%
Matches 94; Conservative
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                             [2]
SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
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Best Local S
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Q8TCD0
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X Studbards From N.B.

X Straubberg R.L.; Peingold E.A.; Grouse L.H., Derge J.G.;

A Straubberg R.L.; Peingold E.A.; Grouse L.H., Derge J.G.;

A Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

A Altschul S.F.; Joederg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

A Diatchenko L.; Marusina K.; Farmer A.H.; Rubin G.M.; Heiseh F.;

A Diatchenko L.; Warusina K.; Farmer A.H.; Rubin G.M.; Hong L.;

A Diatchenko L.; Usdin T.B.; Toshiyuki S., Carninol E., Scheetz T.E.;

B Drownstein M.J.; Usdin T.B.; Toshiyuki S., Carninol E., Prange C.;

A Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

B Boak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

R Richards S., Worley K.C.; Hale S., Garcia A.M.; Gay L.J.; Hulyk S.M.;

A Nilalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Khiting M., Madan A.; Young A.C.; Shevchenko Y.; Bouffaus G.G.;

A Mitting M., Madan A.; Young A.C.; Shevchenko Y.; Bouffaus G.G.;

A Rakeeley R.W.; Touchman J.W.; Offene E.D.; Dickson M.C.;

A Rakeeley R.W.; Touchman J.W.; Carean E.D.; Dickson M.C.;

A Rakeeley R.W.; Touchman J.W.; Schmutz J.; Myers R.M.; Butterfield Y.S.;

Krzywinski M.I.; Skalska U.; Smailus D.E.; Schnerch A.; Schein J.E.;

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 YQQKPGQAPRLLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRLPAQLLGLLMLWVSGSSGDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDW 60
                                                                                                                                                                                                                                                                                                                                                                                                          1 METPAQLIFLILIMIPDITGEIVLIQFPGTLSLSPGERATLSCRASQSVASA----YLAW
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical Corean (Human).
Eukaryota Metazoa (Hordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                .,
2
                                                                                                                                                                                                                                                                                                                                                Length 239;
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                                                                            to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                  F5E20AD3B0552C0A CRC64;
                                                                                                                                                                                                                                                                                                                                              62.4%; Score 460.5; DB 4;
llarity 62.6%; Pred. No. 6.8e-39;
Conservative 22; Mismatches 28;
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                                                                                                                                                                                                                 Pfam: PF00047; Igr. 2—.
SMART; SM00407; Igr. 1.
SMART; SM00406; IGc. 1.
PROSITE; PS50835; IGL LIKE; 2.
PROSITE; PS00209; IG MHC; 1.
Hypothetical protein.
SEQUENCE 239 AA; 26024 MW; F5
                                                           Strausberg R.; Strausberg R.; Submitted (JTV 2002) to the EMB EMBL; BC030814; AAH30814.1; -- PIR; S23638; S23638. PIR; S43991; S34091. PIR; S40357; S40357. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig MFC. InterPro; IPR003596; Ig MFC. InterPro; IPR003596; Ig MFC. InterPro; IPR003596; Ig MFC.
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                               SEQUENCE FROM N.A.
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   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 MRVLAQLIGILLICFPGARCDIQMTQSPSSLSASVGDTVTITCRASQDI-SNYLAWFQQK 61
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                       7
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                                                                                                                                                                                                                                                                                                         Length 236;
                                                                                                                                                                                                                                                                                                              61.7%; Score 455; DB 4; Length 23, 65.7%; Pred. No. 2.5e-38; arive 16; Mismatches 31; Indels
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Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005332; AAH05332.1;
Hypothetical protein.
SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-07N-2002 (TrEMBLrel. 21, Created)
01-07N-2002 (TrEMBLrel. 21, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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MEDLINE=2238827; PubMed=12477932;
A Klausher K.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
A Klausher R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
A patchench L., Marusha K., Farmer A.A., Rubin G.W., Horge L.,
A patchench M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Yilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Nadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Barkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Chriguez A.C., Grimwood J., Schmuzz J., Myers R.M., Butterfield Y.S.,
A Understion and initial analysis of more than 15,000 full-length human
and mouse C.D.A sequences F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 APRILLIYGASSRATDIPHRESGSGSTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LLPILMLWLQGSYGQIVLTQSPDYVSVSPGETVTLTCKASSSVAIGSTIYLHWYQQKSGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASOSVA---SAYLAWYQQKPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bux musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 11 TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 56.6%; Score 418; DB 13; Length 237; Local Similarity 62.9%; Pred. No. 1.5e-34; es 88; Conservative 16; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein S., Strausberg R.;
Submitted (JUN 2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054155; AAHS4155.1; -.
Hypothetical protein Protein Protein SEQUENCE 237 AA; 26300 MW; 47BBDDD2639CB436 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 TKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRVELKRNDAKPAVFIFKPS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B32248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Q99M37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 EIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQKPGQAPRLLIYGASSRATDIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BIVWTQSPATLSVSPGERATLSCWASQSI-SSNLAWYQQKPGQAPRLLIYGASTRATGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'SZ36;
01-0CT-2003 (TYENBLrel. 25, Last sequence update)
01-0CT-2003 (TYENBLrel. 25, Last sequence update)
101-0CT-2003 (TYENBLREL. 25, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Whole;
MEDLINE=22341132; PubMed=12454917;
Klain S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 HRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARFSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.,
                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                          109 AA.
PSTFGQGTKLEIKRTVAAPSVFIFPPS 146
                                                                                                                                                       Created)
                                                                                                          PRT;
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F32530. PH1042. PH1043. PH1044.

PH1043; PH1044;

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4; Gaps

63 99

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57 YQQXPGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 -YLQKPGQSPKILIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQ-STHV 118
                                                                                                                                                                                                                                                                                                                                                                                                                       1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSV----ASAYLAW
                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).

Homo sapiens (Human).

Eukarycis, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                               Query Match 56.0%; Score 413; DB 11; Length 238; Best Local Similarity 55.8%; Pred. No. 4.8e-34; Matches 82; Conservative 28; Mismatches 31; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AR038031, AAD$6667.1; -.
PIR, B30609; B30609.
PIR, C30609; C30609.
PIR, S34099; S34099.
PIR, S34099; LWTL.
InterPro; IPR03596; Ig_v.
Frank, PR00047; 19; 1.
SWART; SMO0406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 LLIFGGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 PPTFGGGTKLEIKRADAAPTVSIFPPS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                  InterPro; IPR000110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfan; PR00047; ig; 2
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                            SMART; SM00406; ĬĠv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                             PH1030.
PH1031.
PH1034.
                                                                                                                                                             S26334; S26334
S53750; S53750
                                                                                                                                               S16112
                                                                                                                                                                                      S60066; S60066
                                                                           PH1031; PH1034; PL0257; PT0359; PT0359; S07455; S16112;
                                                          PH1030;
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       RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQ-GSHV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSV----ASAYLAW 56
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                           Query Match 56.2%; Score 415; DB 11; Length 238; Best Local Similarity 55.8%; Pred. No. 3e-34; Matches 82; Conservative 28; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 PYTFGSGTKLEIKRADAAPTVSIFPPS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 LLTFGGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
Strausberg R.;
Submitted (UBC-2001) to the EN EMBL; BC019760, AAH19760.1; --
PIR; A22687, A2264.
PIR; A322487, A32248.
PIR; B30577, B30577.
PIR; B312487, B30577.
PIR; B41940, B41940.
PIR; C32248, C32248.
PIR; C32248, C32248.
PIR; C32248, C32248.
PIR; C32248, C32348.
PIR; C32248, C32348.
PIR; C32248, C32348.
PIR; C32248, C32348.
PIR; D29380, D29380.
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Q8VCI6
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01-OCT-2002
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Q8K0F8;
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                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 MRTPAQFLGILLLWFPGMKCDIKMTQSPSSMYASLGERVTITCKASQDI-NSYLSWFQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 PGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFP-RTF
                                                                                                 21 EIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQKPGQAPRLLIYGASSRATDIP
                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Musin
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93383497; PubMed=8372513;
Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
Cloning and characterization of 1116N919.9 heavy and light chain cDNAs and expression of antibody fragments in Escherichia coli.";
Year Immunol. 7:56-62 (1993).
EMBL; S65921; AAB28160.1; -.
SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA10F4C CRC64;
                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                          ARFSGSGSGTEFTLTISSLOFEDFAVYYCQHYNNWP-FTFGPGTKVDIKR 108
                                                                                                                                             81 HRFSGSGGGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.1%; Score 407; DB 11; Length 236; 55.9%; Pred. No. 2e-33; ative 23; Mismatches 38; Indels ;
                                                     Length 108;
                                                                            Indels
                                 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-colorectal carcinoma light chain.
                                                     Score 411; DB 4; L. Pred. No. 2.8e-34; 7; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 AA.
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STRAIN-CZECH II, TISSUE-Breast tumor;
MEDLINE-22388257; Pubmed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTKLEIKRADAAPTVSIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                        PRT;
                                11834 MW;
 PS50835; IG_LIKE; 1.
                                                     55.7%;
ilarity 78.2%;
Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                         PRELIMINARY;
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                      108
                                         Query Match
Best Local Similarity
Thes 86; Conserve
                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                     108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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          NON TER
NON TER
SEQUENCE
PROSITE;
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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., More T., Max S.L., Wang J., Heiseh F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleron M., Soarse M.B., Bonaldo M.F., Casrvinci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McZewan F.J., McKernan K.J., Malke J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

""Generation and initial analysis of more than 15,000 full-length human
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Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Muscaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, MuschI_TaxID=10090;
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Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC031498; AM131498.1;
R PIR, A33933; A33933.
R PDB; IKN2; 13-MAR-02.
CO; GO:0016491; F:oxidoreductase activity; IEA.
R CO; GO:0015491; F:oxidoreductase activity; IEA.
R InterPro; IPR002198; ADH_short.
R InterPro; IPR003199; IG.
R InterPro; IPR003109; IG.
R InterPro; IPR003109; IG.
R InterPro; IPR003597; IG.
R InterPro; IPR003509; IG.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
EMBL: BC055906; AAH55906.1; -
Hypotherical protein.
SEQUENCE 236 AA; 26299 MW; ODB03488AAA6396F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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54.7%; Score 404; DB 11; 1
Best Local Similarity 56.6%; Pred. No. 4e-33;
Matches 81; Conservative 21; Mismatches 39;
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STRAIN-CZECH II, TISSUE-Breast tumor;
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(TrEMBLrel. 22, I
(TrEMBLrel. 25, I
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Search completed: April Job time: 30,4873 secs

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60 QGKSPQLLVYNAKTLADGVPSRFSGSRSGTQFSLKINSLQPEDFGSYYCQHH-SGIPFTF 118
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Mammalia; Butheria; Rodentia; Sciurognathi; Murídae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; BC019474; AAH19474.1; -.
REMBL; BC019474; AAH19474.1; -.
RINterPro; IPR007110; Ig-like.
RINterPro; IPR007106; Ig-like.
RINterPro; IPR007306; Ig-V.
R Pfam; PF00047; Ig. 2.
R SMART; SM00406; IgV; 1.
R PROSITE; PS00209; IG_MKC; 1.
R PROSITE; PS00209; IG_MKC; 1.
R Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
                                                                                                                                                                                Query Match 52.9%; Score 390.5; DB 11; Length Best Local Similarity 55.1%; Pred. No. 9.7e-32; Matches 81; Conservative 24; Mismatches 37; Indels
InterPro; IPR003596; Ig_v.

Pfam; PP00047; Ig; 2.

SMART; SM00407; IG; 2.

SMART; SM00407; IGc1; 1.

SMART; SM00407; IGc1; 1.

PROSITE; PS00061; Abh SHORT; 1.

PROSITE; PS00061; IG_IKE; 2.

PROSITE; PS00280; IG_MHC; 1.

Hypchherical protein.

SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8VCPO;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
10-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
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Best Local Similarity
Matches 80; Conserv
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                                                                   (without alignments) . 874.270 Million cell updates/sec
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                                                                                               US-10-044-569B-8
738
1 METPAQLLFLLLLMLPDTTG......TKVEIKRTVAAPSVFIFPPS 143
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                                                        April 5, 2004, 12:09:21 ; Search time 46.2149 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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26 609 82.5 236 4 AAG71272 29 604 81.8 134 2 ABG63490 29 604 81.8 134 2 AAR3672 30 602.5 81.6 129 2 AAR3672 31 595.5 80.4 129 2 AAR3672 32 585 79.3 234 5 AAC1406 33 583.5 79.3 129 2 AAR41286 35 583.5 79.1 129 2 AAR41286 36 580.5 79.1 129 2 AAR41286 36 580.5 79.1 129 2 AAR3101 37 580.5 79.1 129 2 AAR3101 38 575.5 78.0 384 4 AAU14461 41 575.5 78.0 384 4 AAU14461 42 575.7 77.9 226 4 AAB99397 45 575 77.9 226 4 AAB99397	Aag71272 Human gen	_	0 Anti	_	Aar38672 vk325-Jk2		Aao14066 Light cha			Add01357 Human imm	Aar38673 F105Vk-F1	Human	Aau33249 Novel hum	Aau14462 Human nov	Aau14463 Human nov	Aau14461 Human nov	Aaul4464 Human nov	ω	Aab75011 Anti-IL8	Aab99397 Human int	
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0 00 000000000000000000000000000000000	82.5	82.5	82.3	81.8	81.6	80.4	79.3	79.3	79.1	79.1	78.7	78.4	78.0	78.0	78.0	78.0	78.0	77.9	77.9	77.4	
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	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

Monoclonal antibody; variable region; heavy chain; light chain; VH; VL; complementarity determining region; CDR; MAb; BO2C11; conformational bepicop; factor VIII; KRXII; von Willebrand factor; hemostasis; intravascular coagulation; arterial thrombosis; arterial restenosis; venous thrombosis; arteriosclerosis. Novel cell lines for producing monoclonal antibodies that bind to a factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders. Light chain variable region VL of KRIX1. Location/Qualifiers AAB47061 standard; protein; 143 AA 43. .54 /label= CDR1 69. .75 /label= CDR2 Jacquemin MG, Saint-Remy JR; 13-JUL-2000; 2000WO-EP006677 99GB-00016450 99US-0143891P (LEUV-) LEUVEN RES & DEV VZW 109. .118 /label= CDR3 (first entry) WPI; 2001-138333/14. N-PSDB; AAC85454. WO200104269-A1 14-JUL-1999; 14-JUL-1999; Homo sapiens 08-MAY-2001 18-JAN-2001 AAB47061; Key Domain Domain Domain AAB47061

Example 5; Fig 9; 55pp; English

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N-PSDB; AAL49257
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This sequence represents the light chain variable region of the monoclonal antibody (RMD), KRIXI. This MAD produced by the cell line of the invention, specifically recognises the wild type factor VIII light chain. KRIXI can be used to inhibit the binding of factor VIII light willebrand factor in a dose dependant manner. The new cell line KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder or thrombosic pathologic condition such as intravascular coagulation, arterial thrombosis, arterial restenosis, venous thrombosis or arteriosclerosis, and attenuation of coagulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly
                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, antibody; BO2CII; KRIXI; light chain; heavy chain; inflammation; variable region; factor VIII inhibitor; sepsis; septic shock; thrombus formation; systemic inflammatory response syndrome; CDR, disseminated intravascular coagulation; haemophilia A; immunosuppressive; complementarity determining region; antibacterial; antiinflammatory.
                                                                                                                                                                                                                                                                                                    PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLF 120
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                                                                                                                                                                                           100.0%; Score 738; DB 4; Length 143; 100.0%; Pred. No. 3e-47; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human KRIX1 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                  GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   GGGTKVEIKRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                               AAO18879 standard; protein; 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 .54
/label= CDR1
69. .75
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COLL-) COLLEN RES FOUND VZW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2002; 2002EP-00447005.
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/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                         Local Similarity 100.
nes 143; Conservative
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                                                                                                                                                                        Sequence 143 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1222929-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                     Matches 143;
                                                                                                                                                     in humans
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                                                                                                                                                                                               Query Match
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AAO18879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; light chain; 24-2-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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Pharmaceutical composition for treating systemic inflammatory response syndrome, sepsis, septic shock and/or thrombus formation in mircrovasculature in mammals, comprises a partial inhibitor of factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 METPAQLIFLLLLWIPDTTGEIVLTQFPGTLSISPGERATISCRASQSVASAYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 738; DB 5; Length 143; 100.0%; Pred. No. 3e-47; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTKVEIKRTVAAPSVFIFPPS 143
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                                                                                                                                                                                          Disclosure; Fig 13; 41pp; English.
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Best Local Similarity 100.
Matches 143; Conservative
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N-PSDB; ADE28480.
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RESULT 5
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                                                     The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody the invention demonstrates cytostatic, virunide, antibacterial, immunostimulant and anti-HIV such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length light chain protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1 METPAQLIFILLIMIPDITGEIVLIQFPGTLSISPGERATISCRASQSVASAYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                    Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                 Score 667; DB 7; Lt
Pred. No. 8.3e-42;
3; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The kappa chain of immunoglobulin clone 4.1.1.
                      Claim 7; SEQ ID NO 88; 177pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPGTKVDIKRTVAAPSVFIFPPS 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93702 standard; protein; 235 AA.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              Sequence 234 AA;
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The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA) -4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FR1-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to thinbib trans-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to used to up-regulate immune system to up-regulate immune system to up-regulate immune system to up-regulate immunodeficient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                       90.3%; Score 666.5; DB 3;
ilarity 91.6%; Pred. No. 9.1e-42;
Conservative 5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The kappa chain of immunoglobulin clone 4.1.1.

    .20
    note= "signal peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GGGTKVEIKRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOGTKVEIKRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93729 standard, protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US030895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-442647/38.
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA46893.
                                                                                                                                                                                                                                                                                                                                           Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200037504-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1998;
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Corvalan JR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-2000
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Matches 131;
                                                                                                                                                                                                                                                                                       disorders
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Best Local S
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         The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antiplen (CTLA) antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity discrete autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to used to up-regulate immune system to up-regulate immune disease.
                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                   PGQAPRILIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                         1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK 60
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                                                                                                                                                                                                                                                                                                                                                               PGQAPRILIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSP-WTF
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the preparation of medicament for the treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Mature anti-CTLA-4 antibody kappa chain"
                                                                                                                                                                                                                                               .;
H
                                                                                                                                                                                                                 Length 235;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                 Score 666.5; DB 3;
Pred. No. 9.1e-42;
5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-CTLA-4 antibody kappa chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .20
/label=_Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                              143
                                                                                                                                                                                                                                                                                                                                                                                                                         120 GOGTKVEIKRTVAAPSVFIFPPS 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE35884 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2001; 2001US-0293042P.
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                                                                                                                                                                                                               Query Match
Best Local Similarity 91.6%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1G; 76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mueller EE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-131215/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD54344.
                                                                                                                                                                                        Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human 4.1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
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PGQAPRLLIYGASSRATGIPDRFFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSP-WTF 119
                                                                                                                                                                                                                                                                                                                   PGQAPRILITYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
The invention relates to the use of human anti-cytotoxic T lymphocyte antigen-4 (anti-CTLA.4) antibody in the preparation of a medicament for the treatment of cancer such as bone cancer, pancreatic cancer, skin cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian cancer, cancer of the anal region, stomach cancer, breast cancer, cesticular cancer and carcinoma of the fallopian tubes. The present sequence is human anti-CTLA-4 antibody kappa chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; hepatotropic; activation inducible lymphocyte immunomodulatory molecule; AILIM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; graft versus host reaction; immune rejection; intestinal immunity; ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel human antibody (I), preferably a human
                                                                                                                                                                                                                                                                    1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-human AILIM monoclonal antibody clone Jmab-138, light chain.
                                                                                                                                                                                                                1;
                                                                                                                                                                              Length 235;
                                                                                                                                                                                                              Indels
                                                                                                                                                                            Score 666.5; DB 6;
Pred. No. 9.1e-42;
5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 30; Page 284-285; 300pp; English
                                                                                                                                                                                                                                                                                                                                                                                          GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                        120 GOGTKVEIKRTVAAPSVFIFPPS 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU74299 standard; protein; 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-2000; 2000JP-00147116.
30-MAR-2001; 2001JP-00099508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LS-MAY-2001; 2001WO-JP004035
                                                                                                                                                                            Query Match
Best Local Similarity 91.6%;
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuji T, Tezuka K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-075313/10.
N-PSDB; AAS99475.
                                                                                                                                            Sequence 235 AA;
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monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (1) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cyrokine from AILIM-expressing cells, for inducing antibody-dependent cytotoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells, and/or immune cytolysis or apoptosis of AILIM-expressing cells. (1) is useful for treating, preventing or ransduction, and for inhibiting the onset and/or advancement of the prophylaxis of delayed type allergy. (1) is useful for treating and prevention and/or treatment of the contact-type dermatitis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, pooriasis, autoimmune or allergic disorders, inflammatory dermatosis, pooriasis, autoimmune or allergic disorders, inflammatory disorders of the the invention intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatitis. (1) induces no serious antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-mouse antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-munen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 METPAQLIFILILIMIPDTTGEIVLTQSPGTLSLSPGERATLSCRASQNIRSSYLAMYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Osteoprotegerin ligand, osteopathic, antiinflammatory, antirheumatic, antiarthritic, cytostatic, OPGL, anti-OPGL-1, antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               89.4%; Score 660; DB 5; L
88.8%; Pred. No. 2.8e-41;
live 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .20
/note= "IgG2 signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "variable region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-OPGL-1 antibody kappa light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOGTKLEIKRTVAAPSVFIFPPS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2001; 2001US-0301172P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.8
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003002713-A2
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVFYCQQYGSSP-RTF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                         New antibodies that interact with osteoprotegerin ligands, useful for treating osteopenic disorders, e.g. osteoporosis, bone loss from arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 METPAQLIFILILIMEDITIGEIVLTQSPGTLSLSPGERATLSCRASQSVRGRYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 METPAQLLFLLLUMLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; variable region; heavy chain; light chain; VH; complementarity determining region; CDR; MAb; BO2CII; conformational epitope; factor VIII; KRIXI; von Willebrand factor; hemostasis; intravascular coagulation; arterial thrombosis; arterial restenosis; venous thrombosis; arteriosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 658.5; DB 6; Length 235;
Pred. No. 3.6e-41;
2; Mismatches 9; Indels 1;
                                              g,
                                              Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain variable region VL of BO2C11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GQGTKVEIKRTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                              Corvalan JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB47060 standard; protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                   Claim 1; Fig 4; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43. .54
/label= CDR1
69. .75
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109. .117
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.2%;
91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.6
Matches 131; Conservative
                                              Boyle WJ, Martin FH,
(ABGE-) ABGENIX INC. (AMGE-) AMGEN INC.
                                                                                WPI; 2003-210262/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       kappa light chain
                                                                                                  N-PSDB; ABZ59148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 235 AA;
                                                                                                                                                                                    osteonecrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB47060;
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The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic inflammatory response syndrome (SIRS), sepsis, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an active ingredient a partial inhibitor of factor VIII, in admixture with a carrier. Such inhibitors may include the antibodies BO2CII and KRIXI. The present sequence is the light chain variable region of BO2CII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLLFLLLLWLPDTTGBIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical composition for treating systemic inflammatory respons syndrome, sepsis, septic shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor
complementarity determining region; antibacterial; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.7%; Score 654.5; DB 5;
89.5%; Pred. No. 4.4e-41;
ive 7; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The kappa chain of immunoglobulin clone 4.8.1.
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 11; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGTKVEIKRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOGTRLEIKGTVAAPSVFIFPPS
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                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                   69. .75
/label= CDR2
108. .116
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                       Saint-Remy JR;
                                                                                                                                                                                                                                                                      11-JAN-2002; 2002EP-00447005.
                                                                                                                                                                                                                                                                                                    11-JAN-2001; 2001US-0261405P.
                                                                                                                                                                                                                                                                                                                                      (COLL-) COLLEN RES FOUND VZW
                                                                                      43. .54
/label≃ CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 89.5
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     2002-610270/66.
                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAL49255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                       Jacquemin MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2000
                                                                                                                                                                                                      EP1222929-A2
                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                      Region
                                                                                                                      Region
                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the light chain variable region of the human monotonal antibody (MAb), BO2C11. BO2C11 is a human MAb which recognises a conformational epitope within the carboxy-terminal of the factor VIII light chain. BO2C11 recognises both the wild type and Arg2150His factor VIII light chains. The MAb produced by the cell line of the invention, KRIXI, specifically recognises the wild type factor VIII light chain. KRIXI, as pecifically recognises the wild type factor VIII light chain. KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with the helpian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolylic agent, are useful for the treament and/or prevention of hemostasis, coaqulation arterial thrombosis, arterial restenois, venous thrombosis or arterisalelersis, and attenuation of coaqulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; antibody; B02C11; KRIX1; light chain; heavy chain; inflammation; variable region; factor VIII inhibitor; sepsis; septic shock; thrombus formation, systemic inflammators: seponse syndrome; CDR; disseminated intravascular coagulation; haemophilia A; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 METPAQLLFLLLMLPDTTGELALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 METPAQLIFILLIMIPDITGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                      Novel cell lines for producing monoclonal antibodies that bind to factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.4e-41; 7; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 654.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human B02C11 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA018877 standard; protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOGTRLEIKGTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                         Example 5; Fig 7; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.5%;
Matches 128; Conservative 7
                                                                                                                                                                                                        Saint-Remy JR;
                                                                                      13-JUL-2000; 2000WO-EP006677
                                                                                                                                                                        RES & DEV VZW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                        WPI; 2001-138333/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 142 AA;
                                                                                                                                                                                                                                                        N-PSDB; AAC85453
                                                                                                                                                                        (LEUV-) LEUVEN
                       WO200104269-A1.
                                                                                                                                                                                                        Jacquemin MG,
                                                                                                                      14-JUL-1999;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-2002
                                                      18-JAN-2001
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Gaps

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4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-liferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                           Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 METPAQLLFLLLLMLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                          Davis CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 233;
                                                                                                                                                                                                                          Gilman SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
 proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 654.5; DB 3;
Pred. No. 7e-41;
2; Mismatches 7;
                                                                                                                                                                                                                    Hanke JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The kappa chain of immunoglobulin clone 4.8.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 GGGTKVEIKRTVAAPSVFIFPPS 140
                                                                                                                                                                                                                          Mueller EE,
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                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 1B; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93731 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.7%;
91.6%;
                                                                                                                    99WO-US030895.
                                                                                                                                                  98US-0113647P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 131, Conservative
                                                                                                                                                                                                                          Neveu MJ,
                                                                                                                                                                                                                                                                    WPI; 2000-442647/38.
N-PSDB; AAA46867.
                                                                                                                                                                             (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 233 AA;
                                                           WO200037504-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                  23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2000
                               Homo sapiens
                                                                                                                    23-DEC-1999;
                                                                                                                                                                                                                        Hanson DC,
Corvalan JR;
                                                                                       29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders
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SXXXXXXXXXXXXXXXX
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The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA) + Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in 10R1, ODR2 and/Or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                                                     Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METPAQLLFILLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                       Davis CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 233;
                                                                                                                                                                                                                       Gilman SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 654.5; DB 3;
Pred. No. 7e-41;
2; Mismatches 7;
                                                                                                                                                                                                                       Mueller EE, Hanke JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 4.8.1 anti-CTLA-4 antibody kappa chain.
                                    /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGTKVEIKRTVAAPSVFIFPPS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTKVEIKRTVAAPSVFIFPPS 143
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 22k; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE35886 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.7%;
91.6%;
                                                                                                                          99WO-US030895
                                                                                                                                                     98US-0113647P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.6
Matches 131; Conservative
                                                                                                                                                                                                                        Neveu MJ,
                                                                                                                                                                                                                                                                WPI; 2000-442647/38.
N-PSDB; AAA46895.
                                                                                                                                                                              (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 233 AA;
                                                                  WO200037504-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                          23-DEC-1999;
                                                                                                                                                     23-DEC-1998;
                                                                                                                                                                                                                        Hanson DC, 1
Corvalan JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-2003
                                                                                              29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
               Key
Peptide
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AAE35886
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ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
AAW40069
ID AAW4
XX
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                                                                      The invention relates to the use of human anti-cytotoxic T lymphocyte antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for the treatment of cancer such as bone cancer, pancreatic cancer, skin cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian cancer, cancer of the anal region, stomach cancer, breast cancer, testicular cancer, uterine cancer and carcinoma of the fallopian tubes. The present sequence is human anti-CTLA-4 antibody kappa chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; hepatotropic; activation inducible lymphocyte immunosucoluatory molecule; ALLIM, monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergy contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; graft versus host reaction; immune rejection; intestinal immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISP-FTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                             Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the preparation of medicament for the treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-human AILIM monoclonal antibody clone Jmab-139, light chain.
                                                21. .233
/note= "Mature anti-CTLA-4 antibody kappa chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 654.5; DB 6; Length
Pred. No. 7e-41;
2; Mismatches 7; Indels
                           1. .20
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTKVEIKRTVAAPSVFIFPPS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGTKVEIKRTVAAPSVFIFPPS 143
             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU74301 standard; protein; 236 AA
                                                                                                                                                                                                                                                                                                Disclosure; Fig 1K; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         88.7%;
91.6%;
                                                                                                                                 23-MAY-2002; 2002EP-00253652
                                                                                                                                                        23-MAY-2001; 2001US-0293042P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 131; Conservative
                                                                                                                                                                              (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                     Mueller EE;
                                                                                                                                                                                                                           WPI; 2003-131215/13.
N-PSDB; AAD54346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-2002
                                                                                 EP1262193-A1
                                                                                                                                                                                                     Hanson DC,
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                                                 Protein
                         Peptide
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The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, for inducing antibody-dependent cytocoxicity against AILIM-expressing cells, (I) is useful for treating, preventing or AILIM-expressing cells. (I) is useful for treating, preventing or prevention, and fessess associated with AILIM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the diseases. (I) is useful for suppression, prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, autolimmune thyroiditis, chronic inflammatory dermatosis, allergic discorders, inflammatory dermatosis, allergic discorders, inflammatory agaft versus psortacist, autolimmune or allergic discorders, immune rejection, disorders caused by abnormal intestinal immunity, specifically inflammatory incomining the profit of the structure or allergic discorders, immune rejection, disorders caused by abnormal intestinal immunity, specifically inflammatory incomining the preference of the service o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AILIM monoclonal antibody amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 88.3%; Score 652; DB 5; Length 23 Best Local Similarity 88.1%; Pred. No. 1.1e-40; Matches 126; Conservative 9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 30; Page 298-299; 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GGGTKVEIKRTVAAPSVFIFPPS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-2000; 2000JP-00147116.
30-MAR-2001; 2001JP-00099508.
                                                                                                                                                                                                                                                                                                           15-MAY-2001; 2001WO-JP004035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hori N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-075313/10.
N-PSDB; AAS99477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 236 AA;
                                                                                                WO200187981-A2.
Homo sapiens.
                                                                                                                                                                                                     22-NOV-2001
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AAW40069;

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This sequence represents the human HII monoclonal antibody variable (V) region heavy (H) chain which specifically recognises the C-antigan. Such an antigen binding fragment may be used for treating a patient with neoplasia. It is especially useful in the detection of lymphomas and leukaemias where the tumour cells bearing the C antigen are circulating in the patients bloodstream. The polymucleotide sequence may be used as a primer or a probe and the encoded protein may be used in a vaccine or for gene therapy. The human monoclonal antibody (MAb), designated HII, specifically recognises cancerous cells. HII is specific for glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma, lung adenocarcinoma, malignant melanoma, colon adenocarcinoma and prostate adenocarcinoma.
                                                                                                     H11; monoclonal antibody; MAD; C-antigen; variable region heavy chain; V region; H chain; neoplasia; detection; lymphoma; tumour call; probe; primer; vaccine; gene therapy; glioblastoma; neuroblastoma; malignant melanoma; adenocarcinoma; small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen binding fragment from monoclonal antibody, H11 - allows tumour specific detection and treatment of neoplasia.
                                                                    Human monoclonal antibody H11 protein variable region H chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 87-88; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                            (NOVO-) NOVOPHARM BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate adenocarcinoma. The detect C-antigen in a sample
                                                                                                                                                                                                                                                                                                       97WO-US008962.
                                                                                                                                                                                                                                                                                                                                         96US-00657449.
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-018515/02.
N-PSDB; AAV10111.
                                                                                                                                                                                                                                                                                                                                                                                                                Maiti PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 150 AA;
                                                                                                                                                                                                                               WO9744461-A2
                                                                                                                                                                                                                                                                                                       22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                           22-MAY-1996;
                                                                                                                                                                                                Homo sapiens
                                    29-MAY-1998
                                                                                                                                                                                                                                                                   27-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                              Dan MD,
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Query Match 88.0%; Score 649.5; DB 2; Length 150; Best Local Similarity 87.7%; Pred. No. 1.1e-40; Matches 128; Conservative 7; Mismatches 8; Indels 3; Gaps

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61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS---AL 117 9 S MEFQAQLIFILIUMLPDITGDIVITQSPGTISLSPGERATLSCRASQSVSSSYLAWYQQK 64 1 METPAQLLFILLIMLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK

65 PGQAPRILIYGASTRATGMPDRFSGSGSGTDFTLIISRLEPEDFAVYCQQYGSSPQTPQ 124

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118 LTFGGGTKVEIKRTVAAPSVFIFPPS 143

Search completed: April 5, 2004, 13:24:17 Job time : 46.2149 secs

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Sequence 8, Appli
Sequence 34, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 15, Appli
Sequence 95, Appli
Sequence 95, Appli
Sequence 95, Appli
Sequence 91, Appli
Sequence 91, Appli
Sequence 91, Appli
Sequence 91, Appli
Sequence 93, Appli
Sequence 91, Appli
                                                                              April 5, 2004, 13:42:12; Search time 33.6328 Seconds (without alignments) 1116.513 Million cell updates/sec
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                                                                                                                                    US-10-044-569B-8
738
1 METPAQLIFLILLMUPDTTG......TKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 US-10-044-5698-8

US-10-153-382-7

US-09-882-3-34

US-10-180-648-4

US-10-044-5698-4

US-10-044-5698-4

US-09-782-337-5

US-09-782-337-5

US-09-782-337-5

US-09-782-337-5

US-09-782-337-5

US-09-782-337-5

US-09-782-337-5

US-10-309-762-95

5 US-10-309-764-89

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Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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0448390
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Match Length
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Maximum DB seq
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No.
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Sequence 4, Appli Sequence 2, Appli Sequence 804, App Sequence 805, App Sequence 805, App	**************************************	equence 37 equence 40 equence 25 equence 10
5-108A-2 1-148-2 1-265-8 1-265-8	10-291-265-80 09-453-234-40 09-453-234-40 09-453-234-86 09-453-234-86 09-453-234-82 10-304-82 10-304-82 10-304-82 10-309-65-33 10-309-67-32 10-30	-309-764-9 -453-234-4 -443-466A-
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779.3	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	74.4 73.9 73.6
	20 20 20 20 20 20 20 20 20 20 20 20 20 2	
4444 644 644 644		4 4 4 4 2 2 4 5

ALIGNMENTS

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US-LIC-V44-D59B-5
Sequence 8, Application US/10044569B
Fublication No. US20030175268A1
Fublication No. US20030175268A1
Fublication No. US20030175268A1
GENERAL INFORMATION:
APPLICANT: D. Collen Research Foundation vzw
APPLICANT: Jacquemin, Marc G
APPLICANT: Saint-Remy, Jean-Marie R
TITLE OF INVENTION: Method and pharmaceutical composition for preventing
TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
FILE REFERENCE: C1968
TITLE OF INVENTION: UNBER: US/10/044,569B
CURRENT FILING DATE: 2002-01-11
FRIOR APPLICATION NUMBER: US 60/261,405
FRIOR APPLICATION NUMBER: US 60/261,405
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 8
SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
LOCATION: (325)..(354)
CTHER INFORMATION: complementary determining region number three
US-10-044-5698-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1277). (162)
OTHER INFORMATION: complementary determining region number one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (205)..(225)
OTHER INFORMATION: complementary determining region number two
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100.0%; Score 738; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.7e-56;
Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-10-044-569B-8
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Gaps

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Indels

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; ORGANISM: Homo sapiens
US-09-859-053-34
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US-10-044-569B-4
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TYPE: PRT
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APPLICANT: Tacula, Kateunari
APPLICANT: Tacula, Takashi
APPLICANT: Tacula, Kateunari
APPLICANT: Tacula, Kateunari
APPLICANT: Tacula, Kateunari
APPLICANT: Hori, No. US20020102658Aluaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TILE REFERENCE: 06501-07901
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT APPLICATION NUMBER: UP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-06-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE FRAESEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSP-WTF 119
                                                                                                                             61 PGQAPRILIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                      1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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Pred. No. 4.6e-50;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/10153382
Publication No US20030086930A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
TILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
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Patent No. US20020102658A1
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Best Local Similarity 91.6
Matches 131; Conservative
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; ORGANISM: Homo sapiens
US-10-153-382-7
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US-09-859-053-34
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US-10-153-382-7
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Sequence 4, Application US/10044569B;
Publication No. US20030175268A1
GENERAL INFORMATION:
APPLICANT: D. Collen Research Foundation vzw
APPLICANT: Saint-Remy, Jean-Marie R
TITLE OF INVENTION: Method and pharmaceutical composition for preventing
TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
FILE REFERENCE: C1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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  Length 236
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                                                   8; Indels
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Pred. No. 2.2e-49;
2; Mismatches 9
Query Match
89.4%; Score 660; DB 9;
Best Local Similarity 88.8%; Pred. No. 1.7e-49;
Matches 127; Conservative 8; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10180648
Sequence 4, Application US/10180648
Publication No. US2004003353A1
GENERAL INFORMATION:
APPLICANT: Boyle, William J
APPLICANT: Davie, William J
APPLICANT: Davis, C. Geoffrey
TITLE OP INVENTION: Antibodies to OPGL
FILE REPERENCE: 06643.0049-00000
CURRENT APPLICATION NUMBER: US/10/180,648
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: 60/301,172
FRIOR APPLICATION NUMBER: 60/301,172
FRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3:1
SEQ ID NO 4
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91.6%;
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US-10-180-648-4
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Best Local Similarity
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118 GGGTKVEIKRTVAAPSVFIFPPS 140
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US-09-859-053-38
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US-09-782-397-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEFEDFAVYCQKYGTKGTSA-ITF 119
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LOCATION: (325)..(351)
OTHER INFORMATION: complementary determining region number three
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LOCATION: (127)..(162)
OTHER INFORMATION: complementary determining region number
                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (205)..(225)
OTHER INFORMATION: complementary determining region number
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89.5%; Pred. No. 2.9e-49;
Mismatches 7; Indels
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Publication No. US20030086930A1
GENERAL INFORMATION:
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT PILITATION NUMBER: US/10/153,382
CURRENT PAPLICATION NUMBER: 60/293042
PRIOR APPLICATION NUMBER: 60/293042
PRIOR APPLICATION NUMBER: 60/293042
PRIOR APPLICATION NUMBER: 60/293042
PRIOR PILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
PRIOR APPLICATION NUMBER: US 60/261,405
PRIOR FILING DATE: 2001-01-1
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 142
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91.6%;
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Matches 131; Conservative
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Best Local Similarity 89.5
Matches 128; Conservative
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US-10-153-382-11
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LENGIH: 233
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Sequence 38, Application US/09859053;
Patent No. US2002012658A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Teuji, Takashi
APPLICANT: Teuji, Takashi
TITLE OF INVENTION: US20020102658Aluaki
TITLE OF INVENTION: HUMAN WONCCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HUMAN WONCCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HUMAN WONCCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HUMAN WONCCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HUMAN WONCCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HUMAN WONCCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HUMAN CUTTLAL USE THEREOF
FILE REFERENCE: 05501-079001
CURRENT APPLICATION NUMBER: US 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-05-18
SOFFWARE: FESTSEE FOR WINDOWS VETSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGQAPRLLIYGASSRATDIPHRPSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWRARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.3%; Score 652; DB 9; I
88.1%; Pred. No. 8.3e-49;
iive 9; Mismatches 8;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Publication No. US20030021779A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.1
Matches 126; Conservative
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LOCATION: (117)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-833-245-237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ-YGTSALLT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ÞGGAPRLLIYXASXRATGIÞXRFSGSGSGTDFTLTISXLEPEDFAVYCQQRXNWPPXYT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 609; DB 11; Length 236; Pred. No. 4.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Indels
                                                                                                                        Sequence 237, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: HUMAN GENOME Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFRENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/259, 358
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER FO SEQ ID NOS: 2267
SEQ ID NO 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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Best Local Similarity 86.8 Matches 125, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (3)
OTHER INFORMATION: Xaa
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (112)
OTHER INFORMATION: Xaa
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS---AL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 PGQAPRILIYGASTRATGMPDRPSGSGSCTDFTLTISRLEPEDFAVYYCQQYGSSPQTPQ 124
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US-10-153-382-15
US-10-153-382-15
Sequence 15, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PC23019A
CURRENT APPLICATION WUMBER: US/10/153,382
CURRENT APPLICATION NUMBER: US/20/153,382
PRIOR APPLICATION NUMBER: US/20/153,382
SPRIOR FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 15
LENGTH: 234
                     FILING DATE: 13-Feb-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 1997-05-22
ATTORNEY, AGBNT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE, DOCKET VUMBER: 31,943
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.0%; Score 649.5; DB 10;
Best Local Similarity 87.7%; Pred. No. 8.4e-49;
Matches 128; Conservative 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 645; DB 14;
Pred. No. 3.3e-48;
2; Mismatches 9;
       APPLICATION NUMBER: US/09/782,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 LIFGGGIKVEIKRIVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                              LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.9%;
Matches 130; Conservative
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ORGANISM: Homo sapiens
US-10-153-382-15
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61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                61 PGQAPRILIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYG-STPLTF 119
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61 PGQAPRILIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF
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Sequence 93, Application US/10309762

Publication No. US20040018198A1

Publication No. US20040018198A1

Publication No. US20040018198A1

APPLICANT: Gudas, Jean

APPLICANT: Gudas, Jean

APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

FILE REFERENCE: ABGENIX.027A

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 60/337275

FRIOR FILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH. 1.
                                                                                                                                                                                                                                   US-10-309-762-91

US-10-309-762-91

Sequence 91, Application US/10309762

Publication No. US20040018198A1

Publication No. US20040018198A1

Publication No. US20040018198A1

APPLICANT: Galds, Jean

APPLICANT: Foltz, Ian

APPLICANT: ABachisa

APPLICANT: ANICAGE1

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: (AZ IX)

TITLE OF INVENTION: (AZ IX)

TITLE OF INVENTION: (AZ IX)

TURENT APPLICATION NUMBER: US/10/309,762

CURRENT FILING DATE: 2002-12-02

PRIOR PILING DATE: 2001-12-03

PRIOR FILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 91

LENGHH: 127

TYPE: DRA
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80.4%; Score 593; DB 15; Length 127;
Best Local Similarity 91.5%; Pred. No. 5.6e-44;
Matches 118; Conservative 1; Mismatches 8; Indels ;
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/ ORGANISM: Homo sapiens
US-10-309-762-91
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ORGANISM: Homo sapiens
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US-10-309-762-93
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US-10-309-764-89
Sequence 89, Application US/10309764
Sequence 89, Application No. US20030232009a1
Sequence 89, Application No. US20030232009a1
Septication No. US20030232009a1
Septication No. US20030232009a1
APPLICANT: Foltz, Ian
APPLICANT: Babcook, John
APPLICANT: Palathumpat, Raju
APPLICANT: Yang, Xiao-dong
APPLICANT: Yang, Xiao-dong
APPLICANT: Angle Changer, Raju
APPLICANT: Wang, Xiao-dong
TITLE OF INVENTION: TREATING AUTOINMUNE DISEASE AND TRANSPLANT REJECTION
TITLE OF INVENTION: TREATING AUTOINMUNE DISEASE AND TRANSPLANT REJECTION
CURRENT APPLICATION NUMBER: 60/337,276
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 89
LENGTH: 128
LENGTH: 128
LENGTH: 128
LENGTH: 128
LENGTH: 128
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80.4%; Score 593.5; DB 15; Length 128;
Best Local Similarity 91.5%; Pred. No. 5.1e-44;
Matches 118; Conservative 3; Mismatches 7; Indels 1;
                 US-10-300-762-79

Publication No. US20040018198A1

Fublication No. US20040018198A1

Fublication No. US20040018198A1

Fublication No. US20040018198A1

Fublicant: Gudas, Jean

APPLICANT: Gudas, Jean

APPLICANT: Handa, Masahisa

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

FILE REFERENCE: ABGENIX.027A

CURRENT APPLICATION NUMBER: CS/0/337275

FRIOR FILING DATE: 2001-12-03

FRIOR FILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastSEQ for Windows Version 4.0

ERNOTH: 127
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Pred. No. 3.1e-44;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.5%;
Matches 118; Conservative
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US-10-309-764-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), ORGANISM: Homo sapiens
US-10-309-762-95
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Gaps 5

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Sequence 4, Application US/09848812
Sequence 4, Application US/09848812
Fublication No. US20030165507A1
GENERAL INFORMATION:
TOTALS OF INVENTION: Douglas
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
TITLE OF INVENTION: WONGCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
TITLE OF INVENTION NUMBER: US/09/848,832
CURRENT FILING DATE: 2001-05-04
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PRELECT FOR Windows Version 4.0
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                                                                           Query Match

80.2%; Score 592; DB 15; Length 127;
Best Local Similarity 90.7%; Pred. No. 6.8e-44;
Matches 117; Conservative 2; Mismatches 8; Indels 2
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